

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 18, 2005, 05:09:32 ; Search time 3730 Seconds

(without alignments)  
9368.096 Million cell updates/sec

Title: US-09-194-164-13

Perfect score: 918  
Sequence: 1 GAATTCATGAGAAAAAAGCCG.....ATCACCATTAGTGAAGCTT 918

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*  
1: gb\_ests1:\*  
2: gb\_ests2:\*  
3: gb\_hlc:\*  
4: gb\_ests3:\*  
5: gb\_ests4:\*  
6: gb\_ests5:\*  
7: gb\_ests6:\*  
8: gb\_g881:\*  
9: gb\_g882:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	317.6	34.6	584	2	BF664453 602146204
2	315.8	34.4	683	7	CR745461 CR745461
3	314.8	34.3	516	2	AM401728 UI-HF-BKO
4	313.4	34.1	536	2	AM402624 UI-HF-BKO
5	311	33.9	881	5	BQ709375 AGENCOURT
6	310.6	33.8	979	5	BQ709399 AGENCOURT
7	309	33.6	424	2	BF874079 IL3-BT011
8	308.6	33.6	566	2	AM405972 UI-HF-BLO
9	308	33.6	745	4	BI759245 603042678
10	307.8	33.5	433	1	AV647117 AV647117
11	307.8	33.5	504	1	AM405787 UI-HF-BLO
12	307.8	33.5	544	2	AM405787 UI-HF-BLO
13	307.8	33.5	734	4	BG686748 602650717
14	307.8	33.5	793	1	AV646708 AV646708
15	307.8	33.5	926	5	BQ706634 AGENCOURT
16	307.8	33.5	998	5	BQ709245 AGENCOURT
17	306.2	33.4	518	2	AM406576 UI-HF-BLO
18	306.2	33.4	862	4	BG758749 602713108
19	306.2	33.4	1014	5	BM918339 AGENCOURT
20	306	33.3	456	2	AM406451 UI-HF-BLO
21	305.8	33.3	472	2	AM405697 UI-HF-BLO
22	305.8	33.3	603	2	AM404910 UI-HF-BLO
23	304.6	33.2	933	5	BQ711272 AGENCOURT
24	304.2	33.1	526	5	BQ331002 QV3-BT019

25	303.8	33.1	1069	5	BM919414 AGENCOURT
26	303.4	33.1	1153	2	BF663521 602144686
27	303	33.0	441	2	BF914735 IL3-UT011
28	303	33.0	441	2	BF914740 IL3-UT011
29	303	33.0	488	4	BM830796 K-EST0104
30	303	33.0	504	2	BF917294 IL3-UT011
31	303	33.0	529	6	CD708287 EST24814
32	303	33.0	544	2	AM405216 UI-HF-BLO
33	303	33.0	644	2	AM405817 UI-HF-BLO
34	303	33.0	679	6	CD684618 EST1138 h
35	303	33.0	923	5	BQ711051 AGENCOURT
36	303	33.0	974	2	BQ707037 AGENCOURT
37	302.6	33.0	489	2	AM406488 UI-HF-BLO
38	302.6	33.0	579	6	CD707672 EST24199
39	302.4	32.9	865	5	BX357917 BX357917
40	301.8	32.9	976	5	BM914525 AGENCOURT
41	301.4	32.8	978	5	BQ707988 AGENCOURT
42	301	32.8	686	6	CD692160 EST8699 h
43	301	32.8	786	6	CB956522 AGENCOURT
44	301	32.8	917	5	BQ711815 AGENCOURT
45	300.6	32.7	718	6	CB957976 AGENCOURT

#### ALIGNMENTS

RESULT 1  
LOCUS BF664453 584 bp mRNA linear EST 21-DEC-2000  
DEFINITION 602146204F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4309680 5',  
mRNA sequence.

ACCESSION BF664453  
VERSION BF664453.1 GI:11938258  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 584)  
NIH-MGC http://mgs.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)

AUTHORS Contact: Robert Strausberg, Ph.D.  
JOURNAL  
COMMENT Email: cgabbs-remail.nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L1CML183 row: h column: 01  
High quality sequence strop: 584.

#### FEATURES

source

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/db\_xref="taxon:9606"  
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/tissue\_type="primary B-cells from tonsils (cell line)"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_48"  
/note="Organ: B-cells; Vector: pOT7; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

ORIGIN

Query Match	34.6%	Score 317.6	DB 2	Length 584
Best Local Similarity	87.3%	Pred. No. 4e-77		
Matches 363	Conservative 0	Mismatches 44	Indels 9	Gaps 1
QY	15	AACCGTATCGCATCGAGTTGCACCTGCTGTTCTGCTACCCGTGGCGAGGCCGAAAT	74	
Db	17	AAACCCCGAGCCAGCTTCTCTTCCCTCGCTACTCTGGCTCCAGATACACCGAGAAA	76	
QY	75	TGTGTGACGAGATCTCCAGGACCCGCTCTTGTGCTCCAGGGGAAAGACCACTCTC	134	
Db	77	TGTGTGACGAGATCTCCAGGACCCCTGTCTTGTCTCCAGGGGAAAGACCACTCTC	136	
QY	135	CTGCAGGGCCAGTCAGAGTGTATGACAGTACTTAACTCTGTATCCAGAGAAACTCTG	194	
Db	137	CTGCAGGGCCAGTCAGAGTGTATACAGAGCTACTTAACCTGTATCCAGAGAAACTCTG	196	
QY	195	CCAGGCTCCGAGGCTCTCATCTATGTGTGCATCCACGAGGCCACTGGCATCCGAGAC	254	
Db	197	CCAGGCTCCGAGGCTCTCATCTATGTGTGCATCCAGAGGCCACTGGCATCCGAGAC	256	
QY	255	GTTGAGTGGCAGTGGGTCCGGGACAGCTTCACTCTCAACATACAGTACGTGAGACCCTGA	314	
Db	257	GTTGAGTGGCAGTGGGTCTGGGACAGATTCCTCTCAACATACAGTACGTGAGACCCTGA	316	
QY	315	AGATTTTGCAGTGTATTACTGTCCAGCACTATGTGTGCTCAACCTCAGACCTCAAGATCAC	374	
Db	317	AGATTTTGCAGTGTATTACTGTCCAGCACTATGTGTGCTCAACCTCAGACCTCAAGATCAC	367	
QY	375	TTTGGCGGAGAGGACCAAGGTGTGAGATCAACAGAACTGTGGCTGACCATCTGTCT	430	
Db	368	TTTGGCGGAGAGGACCAAGGTGTGAGATCAACAGAACTGTGGCTGACCATCTGTCT	423	

FEATURES	source
RESULT 2	
LOCUS	CR745461
DEFINITION	CR745461 Soares fetal liver spleen INRFS Homo sapiens cDNA clone
ACCESSION	IMAGE971p116 ; IMAGE:128454 5', mRNA sequence.
VERSION	CR745461
KEYWORDS	CR745461.1 GI:51667740
SOURCE	EST.
ORGANISM	Homo sapiens (human)
REFERENCE	Homo sapiens
AUTHORS	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE	1 (bases 1 to 683)
JOURNAL	Biert,L., Heil,O., Hennig,S., Korn,B., Neubert,P., Patsch,E., Peters,M., Radelof,U. and Schneider,D.
COMMENT	I.M.A.G.E. cDNA Clone Collection Unpublished (2004) Contact: Inge Ariart RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany Email: www.rzpd.de RZPD; IMAGE971p116. RZPDLIB; I.M.A.G.E. cDNA Clone Collection; Contact: Inge Ariart RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany Tel: +49 30 32639 100 Fax: +49 30 32639 111 www.rzpd.de
	This clone is available royalty-free from RZPD, contact RZPD (clone@rzpd.de) for further information. Seq primer: M3r, primer sequence: TTTCACACAGGAACAAGCTATGAC. Location/Qualifiers
	1..683

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGP97.P116 ; IMAGE:128434"
/sex="male"
/dev_stage="20 week-post conception fetus"

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/lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Scars fetal liver spleen INFLS"  
 /note="Organ: Liver and Spleen; Vector: pRT3D (Pharmacia)  
 with a modified polylinker; Site\_1: Pac I; Site\_2: Eco RI;  
 1st strand cDNA was primed with a Pac I - oligo(dT) primer  
 [5' AACTGAGAGATTTTAAATTAAGATCTTTTCTTTTCTTTT 3'],  
 double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Pac I and cloned into the Pac I  
 and Eco RI sites of the modified pRT3 vector. Library  
 went through one round of normalization. Library  
 constructed by Bento Soares and M.Fatima Bonafido."

Query Match	34.4%	Score 315.8	DB 7	Length 603
Best Local Similarity	94.7%	Pred. No. 1.3e-76		
Matches 344	Conservative 0	Mismatches 7	Indels 12	Gaps 1
QY	70	GATATTGTGTGA	CGCAGTCTCCAGGACCCCTGTCTTTGTCTCCAGGGGAAAGAGCCACC	129
Db	58	GAATTTGTGTGAG	CGCAGTCTCCAGGACCCCTGTCTTTGTCTCCAGGGGAAAGAGCCACC	117
QY	130	CTCTCCCGCAGGGCC	CAGTCAAGTGTTAGTAGAGCTACTTACCCTGTGTTCCGACGAAA	189
Db	118	CTCTCCCGCAGGGCC	AGTCAAGTGTTAGTAGAGCTACTTACCCTGTGTTCCGACGAAA	177
QY	190	CCTGGCCAGGCTCC	CAAGGCTCTCATCTATATGTGCATCCACGAGGCCACTGGCATTGCCA	249
Db	178	CTGGGCCAGGCTCC	CAAGGCTCTCATCTATATGTGCATCCACGAGGCCACTGGCATTGCCA	237
QY	250	GACAGGTTCAGTGG	CAGTGGGTCCGGGACAGACTTCACTCTACCATCATGTAATCTGGAG	309
Db	238	GACAGGTTCAGTGG	CAGTGGGTCTGGGACAGACTTCACTCTACCATCATGTAATCTGGAG	297
QY	310	CCTGAAGATTTT	CAGTGTATTACTGTACAGAGTATGTAGTCACTCTAGACACTTCAG	369
Db	298	CCTGAAGATTTT	CAGTGTATTACTGTACAGAGTATGTAGTCACTCTAGACACTTCAG	345
QY	370	ATCAGTTTGGCG	CGAGGGACCAAGGTGAGATCAAAAGAACTGTGGCTGCACCATCTGTG	429
Db	346	CTCAGTTTGGCG	CGAGGGACCAAGGTGAGATCAAAAGAACTGTGGCTGCACCATCTGTG	405
QY	430	T	430	
Db	406	T	406	

RESULT 3	AM401728	516 bp	mRNA	linear	EST 16-FRB-2000
LOCUS					
DEFINITION	AM401728	UT-HH-BK0-aaf-f-12-0-UT.r1	NIH_MGC_36	Homo sapiens	CDNA clone
ACCESSION	AM401728	IMAGE:305371	5'		mRNA sequence.
VERSION					
KEYWORDS	AM401728.1	GI:6920414			
SOURCE	EST.				
ORGANISM	Homo sapiens (human)				
REFERENCE	Homo sapiens				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
JOURNAL	1 (bases 1 to 516)				
COMMENT	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .				
	National Institutes of Health, Mammalian Gene Collection (MGC)				
	Unpublished (1999)				
	Contact: Robert Strausberg, Ph.D.				
	Email: <a href="mailto:cgabs@mail.nih.gov">cgabs@mail.nih.gov</a>				
	Eco RI site shown at the beginning of the sequence.				
	Tissue Procurement: Louis M. Staudt, M.D., Ph.D.				
	CDNA Library Preparation: M.B. Soares Lab				
	CDNA Library Arrayed by: M.B. Soares Lab				
	Cloning and Sequencing by: M.B. Soares Lab				
	Clone distribution: MGC clone distribution information can be				
	found through the I.M.A.G.E. Consortium/BLNI at:				
	<a href="http://www-bio.lnl.gov/db/ri/image/image.html">www-bio.lnl.gov/db/ri/image/image.html</a>				
	Seq primer: M13 forward.				

FEATURES  
source

Location/Qualifiers  
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/note="Vector: pT73-Pac; Site 1: NotI; Site 2: Eco RI;  
Constructed from size fractionated cytoplasmic mRNA  
(0.5-1.5kb). Directionally cloned. Cells provided by Louis  
M. Staedt, Ph.D. Library preparation by Maria de Fatima  
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 34.1%; Score 314.8; DB 2; Length 516;  
Best Local Similarity 85.8%; Pred. No. 2,3e-76;  
Matches 362; Conservative 0; Mismatches 57; Indels 3; Gaps 1;

440 GCGGTTCCGAGAGTGTGATCAGTGAAGTGGCTCCAGGTGACGTGTGAGTCTG 499  
93 GGGTTTCTCGTCTCTTTAAGAGGTGTCCAGTGTGACGTGTGAGTCTG 152  
500 GGGAGGCGTGTGTCAGCTGGAGAGTCCCTGAGACTCTCTGTGAGCCTTGATTCC 559  
153 GGGAGGCGTGTGTCAGCTGGAGAGTCCCTGAGACTCTCTGTGAGCCTTGATTCA 212  
560 CTTTCAAGAGCTTTGATGACATGAGTCCGAGGCTTGAAGCAAGGGGCTGAGTGG 619  
213 CTTTCAAGAGCTTTGATGACATGAGTCCGAGGCTTGAAGCAAGGGGCTGAGTGG 272  
620 TGGAGTTATCATATGATGAGACATAAATCTAAGCAGACTCCGTGAAGGGCCGAT 679  
273 TGGAGTTATCATATGATGAGACATAAATCTAAGCAGACTCCGTGAAGGGCCGAT 332  
680 TCACCATCTCCAGAGACACTTCCAGAACACGCGTGTATTAATAATGAACAGCTGAGA 739  
333 TCACCATCTCCAGAGACACTTCCAGAACACGCGTGTATCTGCAATATGAACAGCTGAGA 392  
740 CTGAGAGACAGCGCTGTCTTATCTGTCGAGAGATGAGAGCC---TGTGGGTGACTATG 796  
393 CTGAGAGACAGCGCTGTCTTATCTGTCGAGAGATGAGAGCC---TGTGGGTGACTATG 452  
797 ACCCATCTACAGAGTTGAGCGTCTGAGGCAAGAGGACACGCTCACCGTCTCTCAGAT 856  
453 ACTACTACTACAGAGTTGAGCGTCTGAGGCAAGAGGACACGCTCACCGTCTCTCAGAT 512  
857 CC 858  
513 CC 514

RESULT 4  
AM402624 536 bp mRNA linear EST 16-FEB-2000  
LOCUS  
DEFINITION  
IMAGE:3055359 5', mRNA sequence.  
ACCESSION  
AM402624.1 GI:6921329  
VERSION  
AM402624.1  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
1 (bases 1 to 536)  
NIH-MGC <http://mgi.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-1@mail.nih.gov](mailto:cgapbs-1@mail.nih.gov)

FEATURES  
source

Eco RI site shown at the beginning of the sequence.  
Tissue Procurement: Louis M. Staedt, M.D., Ph.D.  
CDNA Library Preparation: M.B. Soares Lab  
CDNA Library Arrayed by: M.B. Soares Lab  
DNA Sequencing by: M.B. Soares Lab  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/BLN at:  
[www.bio.lnlnl.gov/bird/image/image.html](http://www.bio.lnlnl.gov/bird/image/image.html)  
Seq primer: M3 forward.

ORIGIN

Query Match 34.1%; Score 313.4; DB 2; Length 536;  
Best Local Similarity 85.9%; Pred. No. 5.8e-76;  
Matches 360; Conservative 0; Mismatches 56; Indels 3; Gaps 1;

440 GCGGTTCCGAGAGTGTGATCAGTGAAGTGGCTCCAGGTGACGTGTGAGTCTG 499  
57 GGGTTTCTCGTCTCTTTAAGAGGTGTCCAGTGTGACGTGTGAGTCTG 116  
500 GGGAGGCGTGTGTCAGCTGGAGAGTCCCTGAGACTCTCTGTGAGCCTTGATTCC 559  
117 GGGAGGCGTGTGTCAGCTGGAGAGTCCCTGAGACTCTCTGTGAGCCTTGATTCA 176  
560 CTTTCAAGAGCTTTGATGACATGAGTCCGAGGCTTGAAGCAAGGGGCTGAGTGG 619  
177 CTTTCAAGAGCTTTGATGACATGAGTCCGAGGCTTGAAGCAAGGGGCTGAGTGG 236  
620 TGGAGTTATCATATGATGAGACATAAATCTAAGCAGACTCCGTGAAGGGCCGAT 679  
237 TGGAGTTATCATATGATGAGACATAAATCTAAGCAGACTCCGTGAAGGGCCGAT 296  
680 TCACCATCTCCAGAGACACTTCCAGAACACGCGTGTATTAATAATGAACAGCTGAGA 739  
297 TCACCATCTCCAGAGACACTTCCAGAACACGCGTGTATCTGCAATATGAACAGCTGAGA 356  
740 CTGAGAGACAGCGCTGTCTTATCTGTCGAGAGATGAGAGCC---TGTGGGTGACTATGAC 799  
357 CTGAGAGACAGCGCTGTCTTATCTGTCGAGAGATGAGAGCC---TGTGGGTGACTATGAC 413  
800 ACTACTACAGAGTTGAGCGTCTGAGGCAAGAGGACACGCTCACCGTCTCTCAGATCC 858  
414 ACTACTACAGAGTTGAGCGTCTGAGGCAAGAGGACACGCTCACCGTCTCTCAGATCC 472

RESULT 5  
BQ709375 881 bp mRNA linear EST 16-JUL-2002  
LOCUS  
DEFINITION  
AGENCOURT 7977299 NIH\_MGC\_113 Homo sapiens CDNA clone IMAGE:6215729  
5', mRNA sequence.  
ACCESSION  
BQ709375.1 GI:21848274  
VERSION  
BQ709375.1  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
1 (bases 1 to 881)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)

Tissue Procurement: Dr. Mark Watson  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.lnl.gov>  
Plate: LNCM385 row: b column: 18  
High quality sequence stop: 700.

## FEATURES

## source

1. .881  
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/clone="IMAGE:6215729"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 33.9%; Score 311; DB 5; Length 881;  
Best Local Similarity 93.9%; Pred. No. 3e-75;  
Matches 339; Conservative 0; Mismatches 10; Indels 12; Gaps 1;

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DB 70 GAAATTGTGTGACGAGTCTCCAGGACCCCTGTTCTCCAGGGGAAAGGCCACC 129
QY 130 CTCTCTGCGAGGGCCAGTCAAGTGTAGAGCAGTAACTTACCTGTACAGCAGAAA 189
DB 130 CTCTCTGCGAGGGCCAGTCAAGTGTAGAGCAGTAACTTACCTGTACAGCAGAAA 189
QY 190 CCTGGCCAGGCTCCAGGCTCTCATCTATGTGTCATCCAGGGCCACTGGCATGCCA 249
DB 190 CCTGGCCAGGCTCCAGGCTCTCATCTATGTGTCATCCAGGGCCACTGGCATGCCA 249
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DB 250 GACAGGTTCACTGGGAGTGGGTCCGGGACAGACTTCACTCCATCAGTGAAGTGGAG 309
QY 310 CCTGAAGATTTTGCAGTGTATTACTGTCAAGCAGTATGTAGCTCACTCAGACCTCGA 369
DB 310 CCTGAAGATTTTGCAGTGTATTACTGTCAAGCAGTATGTAGCTCACTCAGACCTCGA 369
QY 370 ATCACTTTGGCGGAGGAGCAAGGTGAGATCAAAAGCAACTGTGGCTGCACCATCTGTC 429
DB 370 ATCACTTTGGCGGAGGAGCAAGGTGAGATCAAAAGCAACTGTGGCTGCACCATCTGTC 429
QY 430 T 430
DB 418 T 418
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RESULT 6  
LOCUS BQ709399 979 bp mRNA linear EST 16-JUL-2002  
DEFINITION AGENCOURT\_797270 NIH\_MGC\_113 Homo sapiens CDNA clone IMAGE:6215847  
ACCESSION BQ709399  
VERSION BQ709399.1 GI:21848298  
KEYWORDS EST.

SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

## REFERENCE

1 (bases 1 to 979)

## AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>.

## TITLE

Unpublished (1999)

## JOURNAL

Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)

## COMMENT

Tissue Procurement: Dr. Mark Watson  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.lnl.gov>  
Plate: LNCM385 row: g column: 16  
High quality sequence stop: 401.

## FEATURES

## source

1. .979  
Location/Qualifiers  
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/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 33.8%; Score 310.6; DB 5; Length 979;  
Best Local Similarity 93.6%; Pred. No. 4e-75;  
Matches 338; Conservative 0; Mismatches 14; Indels 9; Gaps 1;

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QY 70 GATATTGTGTGACGAGTCTCCAGGACCCCTGTTCTCCAGGGGAAAGGCCACC 129
DB 80 GAAATTGTGTGACGAGTCTCCAGGACCCCTGTTCTCCAGGGGAAAGGCCACC 139
QY 130 CTCTCTGCGAGGGCCAGTCAAGTGTAGAGCAGTAACTTACCTGTGATCAGCAGAAA 189
DB 140 CTCTCTGCGAGGGCCAGTCAAGTGTAGAGCAGTAACTTACCTGTGATCAGCAGAAA 199
QY 190 CCTGGCCAGGCTCCAGGCTCTCATCTATGTGTCATCCAGGGCCACTGGCATGCCA 249
DB 190 CCTGGCCAGGCTCCAGGCTCTCATCTATGTGTCATCCAGGGCCACTGGCATGCCA 249
QY 250 GACAGGTTCACTGGGAGTGGGTCCGGGACAGACTTCACTCCATCAGTGAAGTGGAG 309
DB 260 GACAGGTTCACTGGGAGTGGGTCCGGGACAGACTTCACTCCATCAGTGAAGTGGAG 319
QY 310 CCTGAAGATTTTGCAGTGTATTACTGTCAAGCAGTATGTAGCTCACTCAGACCTCGA 369
DB 320 CCTGAAGATTTTGCAGTGTATTACTGTCAAGCAGTATGTAGCTCACTCAGACCTCGA 370
QY 370 ATCACTTTGGCGGAGGAGCAAGGTGAGATCAAAAGCAACTGTGGCTGCACCATCTGTC 429
DB 371 ATCACTTTGGCGGAGGAGCAAGGTGAGATCAAAAGCAACTGTGGCTGCACCATCTGTC 430
QY 430 T 430
DB 431 T 431
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RESULT 7  
LOCUS BF874079 424 bp mRNA linear EST 17-JAN-2001  
BF874079



DEFINITION IL3-ET0115-071100-302-D08 ET0115 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION BP874079  
 VERSION BP874079.1 GI:12264209  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 424)  
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R., Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bala, G. S., Simpson, D. H., Brunstein, A., de Oliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J.  
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 10737800  
 JOURNAL MEDLINE PubMed  
 COMMENT Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=IL3&c2=IL3-ET0115-071100-302-D08&c3=2000-11-07&c4=1)  
 Seq primer: puc 18 forward  
 High quality sequence stop: 392.  
 Location/Qualifiers  
 1..424  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_1ib="ET0115"  
 /note="Organ: lung tumor; Vector: puc18; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."  
 ORIGIN  
 Query Match 33.7%; Score 309; DB 2; Length 424;  
 Best Local Similarity 93.4%; Pred. No. 9, 3e-75;  
 Matches 337; Conservative 0; Mismatches 15; Indels 9; Gaps 1;  
 70 GATATTGTTGACGAGCTCCAGGACCCCTGTCTTTCCTCCAGGGAGAGGCCACC 129  
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 61 GAAATTGTTGACGAGCTCCAGGACCCCTGTCTTTCCTCCAGGGAGAGGCCACC 120  
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 130 CTCTCCTGAGGGGCGAGTGTAGTACAGCTTACCTGCTGGTACAGAGAAA 189  
 |||||  
 121 CTCTCCTGAGGGGCGAGTGTAGTACAGCTTACCTGCTGGTACAGAGAAA 180  
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 190 CTTGACCAAGGCTCCAGGCTCTCATCTATGTTGATCCAGGAGCACTGGCATGCCA 249  
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 181 CTTGACCAAGGCTCCAGGCTCTCATCTATGTTGATCCAGTACGAGCACTGGCATGCCA 240  
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 250 GACAGGTTCAAGGAGGAGTCCGGGAGAGACTTCACTCAACATCAGTACAGTGGAG 309  
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 241 GACAGGTTCAAGGAGGAGTCCGGGAGAGACTTCACTCAACATCAGTACAGTGGAG 300  
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 310 CTTGAGATTTTGCAGTGTATTACTGTACAGAGTATGTTAGCTCACTCAGACACTCG 369  
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 301 CTTGAGATTTTGCAGTGTATTACTGTACAGAGTATGTTAGCTCACTCAGAGG 351  
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QY 370 ATCACTTTGGCGGAGGACCAAGTGGAGATCAACGAACCTGTGGCTGCACCATCTGTC 429  
 |||||  
 DB 352 CTCACCTTTGGCGGAGGAGCAAGGTGGAGATCAACGAACCTGTGGCTGCACCATCTGTC 411  
 |||||  
 QY 430 T 430  
 |||||  
 DB 412 T 412  
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 RESULT 8  
 AM405972  
 LOCUS  
 DEFINITION UT-HF-BLO-2cv-a-01-0-UT r1 NIH\_MGC\_37 Homo sapiens cDNA clone  
 IMAGE:3060360 5', mRNA sequence.  
 AM405972  
 ACCESSION AM405972.1 GI:6925029  
 VERSION AM405972  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 566)  
 NIH-MGC http://mhc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 JOURNAL  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgabbs-remail.nih.gov  
 Eco RI site shown at the beginning of the sequence.  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 cDNA Library Preparation: M.B. Soares Lab  
 cDNA Library Arrayed by: M.B. Soares Lab  
 DNA Sequencing by: M.B. Soares Lab  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNI at:  
 www.bio.lnl.gov/bhrp/image/image.html  
 Seq primer: M13 forward  
 Location/Qualifiers  
 1..566  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone\_1imgb:3060360"  
 /tissue\_type="lymph"  
 /cell\_type="germinal center B cells"  
 /cell\_line="MGC85"  
 /lab\_host="DH10B (UT1)"  
 /clone\_1ib="NIH MGC 37"  
 /note="Vector: pRTT3-Pac; Site\_1: NotI; Site\_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."  
 ORIGIN  
 Query Match 33.6%; Score 308.6; DB 2; Length 566;  
 Best Local Similarity 93.1%; Pred. No. 1, 3e-74;  
 Matches 336; Conservative 0; Mismatches 19; Indels 6; Gaps 1;  
 70 GATATTGTTGACGAGCTCCAGGACCCCTGTCTTTCCTCCAGGGAGAGGCCACC 129  
 |||||  
 66 GAAATTGTTGACGAGCTCCAGGACCCCTGTCTTTCCTCCAGGGAGAGGCCACC 125  
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 130 CTCTCCTGAGGGGCGAGTGTAGTACAGCTTACCTGCTGGTACAGAGAAA 189  
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 126 CTCTCCTGAGGGGCGAGTGTAGTACAGCTTACCTGCTGGTACAGAGAAA 185  
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 190 CTTGACCAAGGCTCCAGGCTCTCATCTATGTTGATCCAGGAGCACTGGCATGCCA 249  
 |||||  
 186 CTTGACCAAGGCTCCAGGCTCTCATCTATGTTGATCCAGGAGCACTGGCATGCCA 245  
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 250 GACAGGTTCAAGGAGGAGTCCGGGAGAGACTTCACTCAACATCAGTACAGTGGAG 309  
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Db 246 GAAGGTTGAGTGGGCTGAGGACAGACTTCACTTCACATCAGACAGACTGAG 305  
QY 310 CTTGAAGATTTTCAGTGTATTAATCTGTACAGAGATGATAGCTACCTCAGACCTCAG 369  
Db 306 CTTGAAGATTTTCAGTGTATTAATCTGTACAGAGATGATAGCTACCTCAGACCTCAG 359  
QY 370 ATACCTTTGGGCGGAGGACCAAGGTGAGATCAACAGACCTGGCTGACCATCTGTC 429  
Db 360 GTACCTTTGGGCGGAGGACCAAGGTGAGATTAACAGACCTGGCTGACCATCTGTC 419  
QY 430 T 430  
Db 420 T 420

RESULT 9  
BI759245 745 bp mRNA linear EST 25-SEP-2001  
LOCUS 603042678F1 NIH\_MGC\_116 Homo sapiens cDNA clone IMAGE:5183010 5',  
DEFINITION mRNA sequence.  
ACCESSION BI759245  
VERSION BI759245.1 GI:15750823  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
TITLE NIH-MGC http://mgc.nci.nih.gov/.  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabds-remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
Plate: LHAM11456 row: 1 column: 19  
High quality sequence stop: 724.  
Location/Qualifiers  
1..745  
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/clone="IMAGE:5183010"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC\_116"  
/note="Organ: pooled colon, kidney, stomach; Vector:  
pCMV-SPORT6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA  
source anonymous pool of 3 colons, age 26 yo male, 49 yo  
female, 71 yo male colon; 46 yo male kidney, and pool of 2  
stomachs; 62 yo male and 70 yo female. Library is  
oligo-dT primed and directionally cloned (EcoRV site is  
destroyed upon cloning). Average insert size 1.4 Kb,  
insert size range 1-3 kb. Library is normalized and  
enriched for full-length clones and was constructed by C.  
Gruber (Invitrogen). Research Genetics tracking code  
023. Note: this is a NIH\_MGC Library."

ORIGIN  
Query Match 33.6%; Score 308; DB 4; Length 745;  
Best Local Similarity 85.8%; Pred. No. 2e-74;  
Matches 357; Conservative 0; Mismatches 50; Indels 9; Gaps 1;

QY 15 AACCGCTATCGGATCGAGTGCAGTGCCTGGTTGCTACCTGGCCAGCCGATAT 74  
Db 21 AAACCCAGGAGGAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 80  
QY 75 TGTGTGAGCAGACTTCAGAGCACCCTGCTTGTCTCCAGGGAAGAGCACCCTTC 134

Db 81 TGTGTGAGCAGACTTCAGAGCACCCTGCTTGTCTCTCTCTCTCTCTCTCTCTCTCT 140  
QY 135 CTGAGGGGCGAGTCAGAGTGTAGTACAGCTACTTACCTGTGTACAGAGAAACCTGG 194  
Db 141 CTGAGGGGCGAGTCAGAGTGTAGTACAGAGCTACTTACCTGTGTACAGAGAAACCTGG 200  
QY 195 CGAGGCTCCGAGGCTCCATCTATGATGATCCAGAGGGGCGACTGGCATGCCAGAG 254  
Db 201 CGAGGCTCCGAGGCTCCATCTATGATGATCCAGAGGGGCGACTGGCATGCCAGAG 260  
QY 255 GTTCAGTGGCAGTGGGTCGAGGACAGACTTCACCTCAGATCAGTAGACAGCTGCA 314  
Db 261 GTTCAGTGGCAGTGGGTCGAGGACAGACTTCACCTCAGATCAGTAGACAGCTGCA 320  
QY 315 AGATTTTCAGTGTATTAATCTGTACAGAGATGATAGCTCAGCTCAGACCTCAGATCA 374  
Db 321 AGATTTTCAGTGTATTAATCTGTACAGAGATGATAGCTCAGCTCAGACCTCAGATCA 371  
QY 375 TTTGCGGCGAGGACCAAGGTGAGATCAACAGACCTGGCTGACCATCTGTC 430  
Db 372 TTTGCGGCGAGGACCAAGGTGAGATCAACAGACCTGGCTGACCATCTGTC 427

RESULT 10  
AV647117 433 bp mRNA linear EST 15-JAN-2002  
LOCUS AV647117 GLC Homo sapiens cDNA clone GLCAUH04 3', mRNA sequence.  
DEFINITION AV647117  
ACCESSION AV647117  
VERSION AV647117.1 GI:9868131  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
TITLE 1 (bases 1 to 433)  
Xiao,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,  
Kuo,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,  
Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,  
Hu,G., Gu,J., Chen,Z. and Han,Z.  
Insight into hepatocellular carcinogenesis at transcriptome level  
by comparing gene expression profiles of hepatocellular carcinoma  
with those of corresponding noncancerous liver  
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)  
21625106  
JOURNAL  
MEDLINE  
PUBMED 11752456  
COMMENT Contact: Zeguang Han  
Chinese National Human Genome Center at Shanghai  
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai  
201203, P. R. China  
Tel: 86-21-50801919(ex.45)  
Fax: 86-21-50801922  
Email: hanzg@chgc.sh.cn  
This clone is available at CHGC in Shanghai.  
Location/Qualifiers  
1..433  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="GLCAUH04"  
/tissue type="corresponding non cancerous liver tissue"  
/dev stage="Adult"  
/lab\_host="SOIR"  
/clone\_lib="GLC"  
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XhoI"

ORIGIN  
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Best Local Similarity 93.4%; Pred. No. 2e-74;  
Matches 337; Conservative 0; Mismatches 12; Indels 12; Gaps 1;

QY 70 GATATTGTGTGAGCAGTTCAGAGCACCCTGCTTGTCTCCAGGGAAGAGCACC 129

Db 83 GAAATGTGTGACGAGCTCTCCAGGACGCTGTCTTTGTCTCCAGGGGAAAAGGCCACC 142

Qy 130 CTCTCTGCAAGGCGCAGTCAAGATGTTAGTACAGCTACTAGCTGGTACGACAGAAA 189

Db 143 CTCTCTGCAAGGCGCAGTCAAGATGTTAGTACAGCTACTAGCTGGTACGACAGAAA 202

Qy 190 CCGGCGCAGGCTCCGAGGCTCCATCTATGTGTGATCCAGCGGGGCCCTGGCAGTCCA 249

Db 203 CTGGCGCAGGCTCCGAGGCTCCATCTATGTGTGATCCAGCGGGGCCCTGGCAGTCCA 262

Qy 250 GACAGTTGAGTGGCAGTGGGTCCGGGAGACATTCATCTCCATCAGTACAGTGGAG 309

Db 263 GACAGTTGAGTGGCAGTGGGTCCGGGAGACATTCATCTCCATCAGTACAGTGGAG 322

Qy 310 CCGAAGATTTTGCAGTGTATTACTGTCAAGCAGTATGTAGTCTACCTGACACCTCAG 369

Db 323 CCGAAGATTTTGCAGTGTATTACTGTCAAGCAGTATGTAGTCTACCTGACACCTCAG 371

Qy 370 ATCACTTTGGCGGAGGAGCAAGGTGAGATCAAGCAAGTGGCTGCACCATCTGTC 429

Db 372 -TCACCTTGGCGGAGGAGCAAGGTGAGATCAAGCAAGTGGCTGCACCATCTGTC 430

Qy 430 T 430

Db 431 T 431

RESULT 11

AV647111 440 bp mRNA linear EST 15-JAN-2002

LOCUS AV647111 GUC Homo sapiens cDNA clone GLCAUG10 3', mRNA sequence.

DEFINITION AV647111

ACCESSION AV647111 GI:9868125

VERSION AV647111.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 440)

AUTHORS Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Pu,G., Zhong,W., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.

TITLE Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

MEDLINE 2165106

PUBMED 11752456

COMMENT Contact: Zeguang Han Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China Tel: 86-21-50801919 (ex.45) Fax: 86-21-50801922 Email: hanzg@chgc.sh.cn This clone is available at CHGC in Shanghai.

FEATURES

source 1..440

location/Qualifiers

1..440

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="GLCAUG10"

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/lab\_host="SOLR"

/clone\_lib="GLC"

/note="Vector: pBluescript sk(-); Site\_1: EcoRI; Site\_2: XhoI"

ORIGIN

Query Match 33.5%; Score 307.8; DB 1; Length 440;

Best Local Similarity 93.4%; Pred. No. 2e-74;

Matches 337; Conservative 0; Mismatches 12; Indels 12; Gaps 1;

Qy 70 GAAATGTGTGACGAGCTCTCCAGGACCTGTCTTTGTCTCCAGGGGAAAAGGCCACC 129

Db 91 GAAATGTGTGACGAGCTCTCCAGGACCTGTCTTTGTCTCCAGGGGAAAAGGCCACC 150

Qy 130 CTCTCTGCAAGGCGCAGTCAAGATGTTAGTACAGCTACTAGCTGGTACGACAGAAA 189

Db 151 CTCTCTGCAAGGCGCAGTCAAGATGTTAGTACAGCTACTAGCTGGTACGACAGAAA 210

Qy 190 CCGGCGCAGGCTCCGAGGCTCCATCTATGTGTGATCCAGCGGGGCCCTGGCAGTCCA 249

Db 211 CTGGCGCAGGCTCCGAGGCTCCATCTATGTGTGATCCAGCGGGGCCCTGGCAGTCCA 270

Qy 250 GACAGTTGAGTGGCAGTGGGTCCGGGAGACATTCATCTCCATCAGTACAGTGGAG 309

Db 271 GACAGTTGAGTGGCAGTGGGTCCGGGAGACATTCATCTCCATCAGTACAGTGGAG 330

Qy 310 CCGAAGATTTTGCAGTGTATTACTGTCAAGCAGTATGTAGTCTACCTGACACCTCAG 369

Db 331 CCGAAGATTTTGCAGTGTATTACTGTCAAGCAGTATGTAGTCTACCTGACACCTCAG 379

Qy 370 ATCACTTTGGCGGAGGAGCAAGGTGAGATCAAGCAAGTGGCTGCACCATCTGTC 429

Db 380 -TCACCTTGGCGGAGGAGCAAGGTGAGATCAAGCAAGTGGCTGCACCATCTGTC 438

Qy 430 T 430

Db 439 T 439

RESULT 12

AW405787 504 bp mRNA linear EST 16-FEB-2000

LOCUS AW405787

DEFINITION UI-HF-BL0-abp-e-02-0-UI.r1 NIH-MGC\_37 Homo sapiens cDNA clone IMAGE:3057482 5', mRNA sequence.

ACCESSION AW405787

VERSION AW405787.1 GI:6924844

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 504)

AUTHORS NIH-MGC http://mgi.nci.nih.gov/.

TITLE NIH-MGC

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

COMMENT Contact: Robert Strusberg, Ph.D. Email: cgaab@-email.nih.gov Eco RI site shown at the beginning of the sequence. Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: M.B. Soares Lab cDNA Library Arrayed by: M.B. Soares Lab DNA Sequencing by: M.B. Soares Lab Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLN at: www.bio.lnl.gov/bbrp/image/image.html Seq primer: M13 Forward.

FEATURES

source 1..504

location/Qualifiers

1..504

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3057482"

/tissue\_type="lymph"

/cell\_type="germinal center B cells"

/cell\_line="MGC85"

/lab\_host="DH10B (LTI)"

/clone\_lib="NIH-MGC\_37"

/note="Vector: pT73-Pac; Site 1: NotI; Site 2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima



FEATURES  
source

Location/Qualifiers  
1. 793  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="GLCAQEO1"  
/tissue\_type="corresponding non cancerous liver tissue"  
/dev\_stage="Adult"  
/lab\_host="SOLR"  
/clone\_11b="GLC"  
/note="Vector: pBluescript sk(-); Site\_1: EcoRI; Site\_2: XhoI"

## ORIGIN

Query Match 33.5%; Score 307.8; DB 1; Length 793;  
Best Local Similarity 93.4%; Pred. No. 2.3e-74;  
Matches 337; Conservative 0; Mismatches 12; Indels 12; Gaps 1;

70 GATATTGTTGACGAGCTCCAGGACCCCTGTCTTGTCTCCAGGGGAAAGCCACC 129  
57 GAAATTGTTGACGAGCTCCAGGACCCCTGTCTTGTCTCCAGGGGAAAGCCACC 116  
130 CTCTCTGACGGGCGCAGTCAAGAGTGTAGTACAGCTACTAGCCCTGTACAGAGAA 189  
117 CTCTCTGACGGGCGCAGTCAAGAGTGTAGTACAGCTACTAGCCCTGTACAGAGAA 176  
190 CTGAGCAGGCTCCAGGCTCTCATCTATGTTGTCATCCAGGCGCATGCCA 249  
177 CTGAGCAGGCTCCAGGCTCTCATCTATGTTGTCATCCAGGCGCATGCCA 236  
250 GACAGGTTCAAGTGGAGTGGTCCGGGAGAGACTTCACTCACTCATGTAAGCTGGAG 309  
237 GACAGATTCAGTGGAGTGGTCTGGGACAGACTTCACTCACTCACTGAGACTGGAG 296  
310 CCTGAAGATTTTGCAGTGTATTACTGTCAAGAGTGTAGTCACTCACTGAGACCTGAG 369  
297 CCTGAAGATTTTGCAGTGTATTACTGTCAAGAGTGTAGTCACTCACTGAGACCTGAG 345  
370 ATCACTTTGGCGGAGGAGCAAGGTGAGATCAAGAGTGTAGTCACTGAGACCTGAG 429  
346 -TCACCTTTCGGGCGGAGGAGCAAGGTGAGATCAAGAGTGTAGTCACTGAGACCTGAG 404  
430 T 430  
405 T 405

RESULT 15  
BO706634 926 bp mRNA linear EST 16-JUL-2002  
LOCUS BO706634  
DEFINITION AGENCOURT\_7975592 NIH\_MGC\_113 Homo sapiens cDNA clone IMAGE:6215094  
5', mRNA sequence.  
ACCESSION BO706634  
VERSION BO706634.1 GI:21845533  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>  
TITLE NIH-MGC  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Dr. Mark Watson  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/ULNL at:  
<http://image.llnl.gov>

Plate: L1CM2383 Row: h Column: 07

FEATURES  
source

High quality sequence stop: 536.  
Location/Qualifiers  
1. 926  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="IMAGE:6215094"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_11b="NIH MGC 113"  
/note="Organ: spleen; Vector: pOT87; Site\_1: XhoI; Site\_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC library."

## ORIGIN

Query Match 33.5%; Score 307.8; DB 5; Length 926;  
Best Local Similarity 93.4%; Pred. No. 2.4e-74;  
Matches 337; Conservative 0; Mismatches 12; Indels 12; Gaps 1;

70 GATATTGTTGACGAGCTCCAGGACCCCTGTCTTGTCTCCAGGGGAAAGCCACC 129  
67 GAAATTGTTGACGAGCTCCAGGACCCCTGTCTTGTCTCCAGGGGAAAGCCACC 126  
130 CTCTCTGACGGGCGCAGTCAAGAGTGTAGTACAGCTACTAGCCCTGTACAGAGAA 189  
127 CTCTCTGACGGGCGCAGTCAAGAGTGTAGTACAGCTACTAGCCCTGTACAGAGAA 186  
190 CTGAGCAGGCTCCAGGCTCTCATCTATGTTGTCATCCAGGCGCATGCCA 249  
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370 ATCACTTTGGCGGAGGAGCAAGGTGAGATCAAGAGTGTAGTCACTGAGACCTGAG 429  
355 CTCACTTTCGGGCGGAGGAGCAAGGTGAGATCAAGAGTGTAGTCACTGAGACCTGAG 414  
430 T 430  
415 T 415

Search completed: February 18, 2005, 08:24:27  
Job time : 3738 secs

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OM nucleic - nucleic search, using sw model

Run on: February 18, 2005, 04:06:26 ; Search time 4372 Seconds  
(without alignments)

10174.265 Million cell updates/sec

Title: US-09-194-164-13

Perfect score: 918  
Sequence: 1 GAATTCATGAAAAAACCAGC.....ATCACCATTAGTAAGCTT 918

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 242267955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*  
1: gb\_ha:\*  
2: gb\_hg:\*  
3: gb\_in:\*  
4: gb\_cm:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_pb:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sgs:\*  
12: gb\_ey:\*  
13: gb\_un:\*  
14: gb\_vl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	918	100.0	918	6	AR139128 Sequence
2	916.4	99.8	918	6	AR139129 Sequence
3	799.6	87.1	867	6	AR139130 Sequence
4	798	86.9	867	6	AR139131 Sequence
5	463.8	50.5	801	12	AF027160 Synthetic
6	445	48.5	1630	6	BD222938 Heteromn
7	445	48.5	1630	6	BD222939 Heteromn
8	445	48.5	1630	6	AX023365 Sequence
9	445	48.5	1630	6	AX023367 Sequence
10	414.4	45.1	867	12	AF416910 Synthetic
11	380.8	41.5	750	6	CQ768475 Sequence
12	369.6	40.3	861	12	AF416909 Synthetic
13	361	39.3	450	6	AR139121 Sequence
14	359.4	39.2	450	6	AR139120 Sequence
15	358.4	39.0	790	10	MMVJ5051 Mus muscu
16	352	38.3	790	10	MMVJ24PRG
17	348.4	37.7	762	6	AX601792 Sequence
18	346.2	37.7	864	12	XXU34924 Synthetic r
19	345.2	37.6	780	12	SYNN19886CF

20	345.2	37.6	783	6	AR198737 Sequence
21	343.6	37.4	786	6	AX601794 Sequence
22	343.6	37.4	1848	6	IT73512 Sequence 15
23	343.6	37.4	1848	12	U06943 Synthetic c
24	342.8	37.3	771	6	AX601793 Sequence
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42	342.8	37.3	771	6	AX601793 Sequence
43	342.8	37.3	771	6	AX601793 Sequence
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#### ALIGNMENTS

RESULT 1	AR139128	918 bp	DNA	linear	PAT 16-JUN-2001
LOCUS	AR139128	Sequence 13 from patent US 6207153.			
DEFINITION	AR139128				
ACCESSION	AR139128.1	GI:14481624			
VERSION					
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 918)				
AUTHORS	Dan, M.D., Maiti, P.K. and Kaplan, H.A.				
TITLE	Antigen binding fragments that specifically detect cancer cells, nucleotides encoding the fragments, and use thereof for the prophylaxis and detection of cancers				
JOURNAL	Patent: US 6207153-A 13 27-MAR-2001;				
FEATURES	location/Qualifiers				
source	1..918				
ORIGIN	/organism="unknown"				
	/mol_type="unassigned DNA"				
Query Match	100.0%; Score 918; DB 6; Length 918;				
Best Local Similarity	100.0%; Pred. No. 5.8e-247; Indels 0; Gaps 0;				
Matches	918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 GAATTCATGAAAAAACCAGCTATCGCATGCGAGTTGCACTGGCTGTTCCGTAACCGTT 60				
DB	1 GAATTCATGAAAAAACCAGCTATCGCATGCGAGTTGCACTGGCTGTTCCGTAACCGTT 60				
QY	61 GCGCAGCGCGATATTGTGTGACGCGATCTCCAGGACCCCTGCTTTGTCTCCAGGGGAA 120				
DB	61 GCGCAGCGCGATATTGTGTGACGCGATCTCCAGGACCCCTGCTTTGTCTCCAGGGGAA 120				
QY	121 AGAGCACCCTCTCTCGAGGGCCGATGAGAGTGTAGAGAGCTACTAGCTGCTGATC 180				
DB	121 AGAGCACCCTCTCTCGAGGGCCGATGAGAGTGTAGAGAGCTACTAGCTGCTGATC 180				
QY	181 CAGCAGAAACCTGGCGAGGCTCCAGGCTCTCATCTATGTGTGATCCAGGAGGCACT 240				
DB	181 CAGCAGAAACCTGGCGAGGCTCCAGGCTCTCATCTATGTGTGATCCAGGAGGCACT 240				



QY 241 GGCATGCCAGACAGGTTTCAGTGGCAGTGGGTCGGGACAGACTTTCATCTCCACCATCACT 300  
|||  
Db 241 GGCATGCCAGACAGGTTTCAGTGGCAGTGGGTCGGGACAGACTTTCATCTCCACCATCACT 300  
QY 301 AGACTGGAGCTGAAGATTTTTCAGTGTATTACTGTACAGAGTATGTTAGTCACTCAG 360  
|||  
Db 301 AGACTGGAGCTGAAGATTTTTCAGTGTATTACTGTACAGAGTATGTTAGTCACTCAG 360  
QY 361 ACACCTCAGATCACTTTCCGCGGAGGACCAAGGTGAGATCAACGAACTGTGGTCA 420  
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Db 361 ACACCTCAGATCACTTTCCGCGGAGGACCAAGGTGAGATCAACGAACTGTGGTCA 420  
QY 421 CCATGTCTCTGGCGGTCGGTCCGAGAGTGTGATCAAGTGAAGTGGTCCCGAG 480  
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Db 421 CCATGTCTCTGGCGGTCGGTCCGAGAGTGTGATCAAGTGAAGTGGTCCCGAG 480  
QY 481 GTGCAGCTGTGAGTCTGGGAGGAGCGTGTCAAGCTGGAGAGTCCCTGAGACTCTCC 540  
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Db 481 GTGCAGCTGTGAGTCTGGGAGGAGCGTGTCAAGCTGGAGAGTCCCTGAGACTCTCC 540  
QY 541 TGTGACGCTCTGAGATTCCTCTTCAGAACTTTGCTATGCACTGGTCCGCAAGCTCTA 600  
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Db 541 TGTGACGCTCTGAGATTCCTCTTCAGAACTTTGCTATGCACTGGTCCGCAAGCTCTA 600  
QY 601 GGCAGAGGAGCTGAGTGGGTGAGATTAATCAATGATGAGAGCACTAAATCACTACGA 660  
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Db 601 GGCAGAGGAGCTGAGTGGGTGAGATTAATCAATGATGAGAGCACTAAATCACTACGA 660  
QY 661 GACTCCGTGAAGGCGGATTCACATCTCCAGAGACATTCGAAAGACGCGTATCTA 720  
|||  
Db 661 GACTCCGTGAAGGCGGATTCACATCTCCAGAGACATTCGAAAGACGCGTATCTA 720  
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Db 721 AAAATGAACAGCTTGAGAACTGAGACAGCGCTGTATTAATCTGTGCGAGATCAAGC 780  
QY 781 CTGTTGGGTGACATATACCACTACGCTTGGAGAGTCTGGGAGCAAGGAGCAACGCTC 840  
|||  
Db 781 CTGTTGGGTGACATATACCACTACGCTTGGAGAGTCTGGGAGCAAGGAGCAACGCTC 840  
QY 841 ACCGTCTCTCAGAGTCCGAAACAAAACATGATCAGGAAAGATCTGAACCATCACT 900  
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Db 841 ACCGTCTCTCAGAGTCCGAAACAAAACATGATCAGGAAAGATCTGAACCATCACT 900  
QY 901 CACCATTAAGTGAAGCTT 918  
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Db 901 CACCATTAAGTGAAGCTT 918

RESULT 2  
AR139129/c 918 bp DNA linear PAT 16-JUN-2001  
LOCUS AR139129  
DEFINITION Sequence 15 from patent US 6207153.  
ACCESSION AR139129  
VERSION AR139129.1 GI:14481625  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 918)  
AUTHORS Dan, M.D., Maiti, P.K. and Kaplan, H.A.  
TITLE Antigen binding fragments that specifically detect cancer cells,  
nucleotides encoding the fragments, and use thereof for the  
prophylaxis and detection of cancers  
JOURNAL Patent: US 6207153-A 15 27-MAR-2001;  
FEATURES Location/Qualifiers  
1..918  
source /organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 99.8%; Score 916.4; DB 6; Length 918;  
Best Local Similarity 99.9%; Pred. No. 1.6e-246;

Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GAATTCATGAAAAAACCGCTATTCGATCGAGTTGCACTGGCTGTGTTGCTAACGTT 60  
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Db 918 GAATTCATGAAAAAACCGCTATTCGATCGAGTTGCACTGGCTGTGTTGCTAACGTT 859  
QY 61 GGGCAGGCGGATTTGTTTGAACGAGTCTCAGGCAACCGTCTTTCCTCCAGGGAA 120  
|||  
Db 61 GGGCAGGCGGATTTGTTTGAACGAGTCTCAGGCAACCGTCTTTCCTCCAGGGAA 120  
QY 858 GGCAGGCGGATTTGTTTGAACGAGTCTCAGGCAACCGTCTTTCCTCCAGGGAA 799  
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Db 858 GGCAGGCGGATTTGTTTGAACGAGTCTCAGGCAACCGTCTTTCCTCCAGGGAA 799  
QY 121 AGAGCAACCTCTCTCGAGAGGCGCAGTCAAGTGTATTAAGTCACTTAAGCTGTATC 180  
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Db 121 AGAGCAACCTCTCTCGAGAGGCGCAGTCAAGTGTATTAAGTCACTTAAGCTGTATC 180  
QY 798 AGAGCAACCTCTCTCGAGAGGCGCAGTCAAGTGTATTAAGTCACTTAAGCTGTATC 739  
|||  
Db 798 AGAGCAACCTCTCTCGAGAGGCGCAGTCAAGTGTATTAAGTCACTTAAGCTGTATC 739  
QY 181 CAGCAAAAACCTGGCCAGGCTCCAGGCTCTCATTAATGTCATCCAGGGGCACT 240  
|||  
Db 181 CAGCAAAAACCTGGCCAGGCTCCAGGCTCTCATTAATGTCATCCAGGGGCACT 240  
QY 738 CAGCAAAAACCTGGCCAGGCTCCAGGCTCTCATTAATGTCATCCAGGGGCACT 679  
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Db 738 CAGCAAAAACCTGGCCAGGCTCCAGGCTCTCATTAATGTCATCCAGGGGCACT 679  
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Db 241 GGCATGCCAGACAGGTTTCAGTGGCAGTGGGTCGGGACAGACTTTCATCTCCACCATCACT 300  
QY 678 GGCATGCCAGACAGGTTTCAGTGGCAGTGGGTCGGGACAGACTTTCATCTCCACCATCACT 619  
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Db 678 GGCATGCCAGACAGGTTTCAGTGGCAGTGGGTCGGGACAGACTTTCATCTCCACCATCACT 619  
QY 301 AGACTGGAGCTGAAGATTTTTCAGTGTATTACTGTACAGAGTATGTTAGTCACTCAG 360  
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Db 301 AGACTGGAGCTGAAGATTTTTCAGTGTATTACTGTACAGAGTATGTTAGTCACTCAG 360  
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Db 618 AGACTGGAGCTGAAGATTTTTCAGTGTATTACTGTACAGAGTATGTTAGTCACTCAG 559  
QY 361 ACACCTCAGATCACTTTCCGCGGAGGACCAAGGTGAGATCAACGAACTGTGGTCA 420  
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Db 361 ACACCTCAGATCACTTTCCGCGGAGGACCAAGGTGAGATCAACGAACTGTGGTCA 420  
QY 558 ACACCTCAGATCACTTTCCGCGGAGGACCAAGGTGAGATCAACGAACTGTGGTCA 499  
|||  
Db 558 ACACCTCAGATCACTTTCCGCGGAGGACCAAGGTGAGATCAACGAACTGTGGTCA 499  
QY 421 CCATGTCTCTGGCGGTCGGTCCGAGAGTGTGATCAAGTGAAGTGGTCCCGAG 480  
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Db 421 CCATGTCTCTGGCGGTCGGTCCGAGAGTGTGATCAAGTGAAGTGGTCCCGAG 480  
QY 498 CCATGTCTCTGGCGGTCGGTCCGAGAGTGTGATCAAGTGAAGTGGTCCCGAG 439  
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Db 498 CCATGTCTCTGGCGGTCGGTCCGAGAGTGTGATCAAGTGAAGTGGTCCCGAG 439  
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Db 438 GTGCAGCTGTGAGTCTGGGAGGAGCGTGTCAAGCTGGAGAGTCCCTGAGACTCTCC 379  
QY 541 TGTGACGCTCTGAGATTCCTCTTCAGAACTTTGCTATGCACTGGTCCGCAAGCTCTA 600  
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Db 541 TGTGACGCTCTGAGATTCCTCTTCAGAACTTTGCTATGCACTGGTCCGCAAGCTCTA 600  
QY 378 TGTGACGCTCTGAGATTCCTCTTCAGAACTTTGCTATGCACTGGTCCGCAAGCTCTA 319  
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Db 378 TGTGACGCTCTGAGATTCCTCTTCAGAACTTTGCTATGCACTGGTCCGCAAGCTCTA 319  
QY 601 GGCAGAGGAGCTGAGTGGGTGAGATTAATCAATGATGAGAGCACTAAATCACTACGA 660  
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Db 601 GGCAGAGGAGCTGAGTGGGTGAGATTAATCAATGATGAGAGCACTAAATCACTACGA 660  
QY 318 GGCAGAGGAGCTGAGTGGGTGAGATTAATCAATGATGAGAGCACTAAATCACTACGA 259  
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Db 318 GGCAGAGGAGCTGAGTGGGTGAGATTAATCAATGATGAGAGCACTAAATCACTACGA 259  
QY 661 GACTCCGTGAAGGCGGATTCACATCTCCAGAGACATTCGAAAGACGCGTATCTA 720  
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Db 661 GACTCCGTGAAGGCGGATTCACATCTCCAGAGACATTCGAAAGACGCGTATCTA 720  
QY 258 GACTCCGTGAAGGCGGATTCACATCTCCAGAGACATTCGAAAGACGCGTATCTA 199  
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Db 258 GACTCCGTGAAGGCGGATTCACATCTCCAGAGACATTCGAAAGACGCGTATCTA 199  
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Db 138 CTGTTGGGTGACATATACCACTACGCTTGGAGAGTCTGGGAGCAAGGAGCAACGCTC 79  
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Db 841 ACCGTCTCTCAGAGTCCGAAACAAAACATGATCAGGAAAGATCTGAACCATCACT 900  
QY 78 ACCGTCTCTCAGAGTCCGAAACAAAACATGATCAGGAAAGATCTGAACCATCACT 19  
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Db 78 ACCGTCTCTCAGAGTCCGAAACAAAACATGATCAGGAAAGATCTGAACCATCACT 19  
QY 901 CACCATTAAGTGAAGCTT 918  
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QY 18 CACCATTAAGTGAAGCTT 1  
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Db 18 CACCATTAAGTGAAGCTT 1

RESULT 3  
AR139130 867 bp DNA linear PAT 16-JUN-2001  
LOCUS AR139130  
DEFINITION Sequence 16 from patent US 6207153.  
ACCESSION AR139130  
VERSION AR139130.1 GI:14481626

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 867)  
AUTHORS Dan, M.D., Maiti, P.K. and Kaplan, H.A.  
TITLE Antigen binding fragments that specifically detect cancer cells,  
nucleotides encoding the fragments, and use thereof for the  
prophylaxis and detection of cancers  
JOURNAL Patent: US 6207153-A 16 27-MAR-2001;  
FEATURES Location/Qualifiers  
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Best Local Similarity 94.0%; Pred. No. 1.2e-213;  
Matches 863; Conservative 0; Mismatches 4; Indels 51; Gaps 1;

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DB 61 GCGCAGGCGCATATGTGTGAACGAGTCTCCAGGCAACCTCTTTGTCTCCAGGGAA 120  
QY 121 AGAGCCACCTCTCTCTGAGGGGCGAGTCAGAGTGTAGTAGAGGCTAGTACCTGGTAC 180  
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QY 361 ACACCTCAGATCACTTTTCGGCGGAGGACCAAGGTGAGATCAACGAACTGTGGCTGCA 420  
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DB 421 TC-----CGAGCAG 429  
QY 481 GTGACGCTGTGAGATCTGGGGGAGCGGTGTCAGCGTGGGAGGTCCTGAGATCTCC 540  
DB 481 GTGACGCTGTGAGATCTGGGGGAGCGGTGTCAGCGTGGGAGGTCCTGAGATCTCC 540  
QY 490 TGTGAGGCTCTGAGATTCCTCTTCAGAAAGCTTGTGTAAGCACTGGGTCCGAGGCTGTA 549  
DB 490 TGTGAGGCTCTGAGATTCCTCTTCAGAAAGCTTGTGTAAGCACTGGGTCCGAGGCTGTA 549  
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QY 661 GACTCCGTGAAGGGCCGATTCAACATCTCCAGAGACATTTCCAGAAACCGGTGATCTTA 720  
DB 661 GACTCCGTGAAGGGCCGATTCAACATCTCCAGAGACATTTCCAGAAACCGGTGATCTTA 720  
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DB 610 GACTCCGTGAAGGGCCGATTCAACATCTCCAGAGACATTTCCAGAAACCGGTGATCTTA 669  
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DB 730 CTGTTGGGTGACTATGACCACTACGAGTTTGAACGTCGTGGGGCAAGGACACGAGTC 789  
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DB 790 ACCGTCTCCTCAGATCCGAAACAAAATGATCAGCAGAAAGATCTGAACCATCAGCAT 849  
QY 901 CACCATTTAGTGAAGCTT 918  
DB 850 CACCATTTAGTGAAGCTT 867

RESULT 4  
AR139131/c 867 bp DNA linear PAT 16-JUN-2001  
LOCUS AR139131  
DEFINITION Sequence 18 from patent US 6207153.  
ACCESSION AR139131  
VERSION AR139131.1 GI:14481627  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 867)  
AUTHORS Dan, M.D., Maiti, P.K. and Kaplan, H.A.  
TITLE Antigen binding fragments that specifically detect cancer cells,  
nucleotides encoding the fragments, and use thereof for the  
prophylaxis and detection of cancers  
JOURNAL Patent: US 6207153-A 16 27-MAR-2001;  
FEATURES Location/Qualifiers  
source 1..867  
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ORIGIN  
Query Match 86.9%; Score 798; DB 6; Length 867;  
Best Local Similarity 93.9%; Pred. No. 3.4e-213;  
Matches 862; Conservative 0; Mismatches 5; Indels 51; Gaps 1;

QY 1 GAATTCATGAAAAAACCCTATCGCATCGCATGTCAGTGGCTGGTTGGCTACCGTT 60  
DB 867 GAATTCATGAAAAAACCCTATCGCATCGCATGTCAGTGGCTGGTTGGCTACCGTT 808  
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DB 807 GCGCAGGCGCATATGTGTGAACGAGTCTCCAGGCAACCTCTTTGTCTCCAGGGAA 748  
QY 121 AGAGCCACCTCTCTCTGAGGGGCGAGTCAGAGTGTAGTAGAGGCTAGTACCTGGTAC 180  
DB 747 AGAGCCACCTCTCTCTGAGGGGCGAGTCAGAGTGTAGTAGAGGCTAGTACCTGGTAC 688  
QY 181 CAGCAGAAACCTGCGCAGGCTCCAGGCTCTCATCTATGTGATCCACAGGGCACT 240  
DB 687 CAGCAGAAACCTGCGCAGGCTCCAGGCTCTCATCTATGTGATCCACAGGGCACT 628  
QY 241 GGCATGCCAGACAGGTTCACTGAGTGGTGGTCCGGGACAGACTTCACTCCACATCACT 300  
DB 627 GGCATGCCAGACAGGTTCACTGAGTGGTGGTCCGGGACAGACTTCACTCCACATCACT 300  
QY 301 AGACTGAGACCTGAGATTTTTCAGTGTATTAATCTGACAGATATGTAGTCACTCAG 360  
DB 301 AGACTGAGACCTGAGATTTTTCAGTGTATTAATCTGACAGATATGTAGTCACTCAG 360  
QY 567 AGACTGAGACCTGAGATTTTTCAGTGTATTAATCTGACAGATATGTAGTCACTCAG 508  
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QY 361 ACACCTCAGATCACTTTTCGGCGGAGGACCAAGGTGAGATCAACGAACTGTGGCTGCA 420  
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QY 421 CCATCTGTCTCTGGGGGTGGCGGTTCCGAGGTGATCAGGTGAGGTGGCTCCAG 480  
DB 447 TC-----CGAGCAG 439  
QY 481 GTGACGCTGTGAGATCTGGGGGAGCGGTGTCAGCGTGGGAGGTCCTGAGATCTCC 540  
DB 438 GTGACGCTGTGAGATCTGGGGGAGCGGTGTCAGCGTGGGAGGTCCTGAGATCTCC 379

QY	541	NTGTGAGCCTCTGGATTTCCCTTTCAAGAGCTTTGCTATGCACTGGGTCGCCAGGCTCTA	600
Db	378	TGTGAGCCTCTGGATTTCCCTTTCAAGAGCTTTGCTATGCACTGGGTCGCCAGGCTCTA	319
QY	601	GGCAAGGGGCTGGAATGGGATGGGAGTATATCATATGATGGAAGCACTAAATACTAACGA	660
Db	318	GGCAAGGGGCTGGAATGGGATGGGAGTATATCATATGATGGAAGCACTAAATACTAACGA	259
QY	661	GACTCCGTGAAGGGCCGATTCACCATCTTCACAGAGACATTCGCAAGAACAGGCTGATCTA	720
Db	258	GACTCCGTGAAGGGCCGATTCACCATCTTCACAGAGACATTCGCAAGAACAGGCTGATCTA	199
QY	721	AAAAAGAACAGGCTTGAGAACTGAGGACACAGGCTGTCTATTAATCTGTCCGAGAGATCAAGC	780
Db	198	AAAAAGAACAGGCTTGAGAACTGAGGACACAGGCTGTCTATTAATCTGTCCGAGAGATCAAGC	139
QY	781	CTGTTGGGTGACTATGACCACTACTACGGTTTGGAAGTCTGGGGGCAAGAGGACCAAGGCT	840
Db	138	CTGTTGGGTGACTATGACCACTACTACGGTTTGGAAGTCTGGGGGCAAGAGGACCAAGGCT	79
QY	841	ACCGTCTCCTCAGATCCGAAACMAAACTGATCAGCGAAGAGATCTGAACCATCACCAT	900
Db	78	ACCGTCTCCTCAGATCCGAAACMAAACTGATCAGCGAAGAGATCTGAACCATCACCAT	19
QY	901	CACCATTAGTGAAAGCTT	918
Db	18	CACCATTAGTGAAAGCTT	1
RESULT 5			
AF027160		801 bp	mRNA linear SYN 06-FEB-2003
LOCUS			
DEFINITION	AF027160	synthetic construct single chain Fv fragment (T6JScFv07)	mRNA,
ACCESSION	AF027160		
VERSION	AF027160.2	GI:23683339	
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REMARK			
COMMENT			
FEATURES			
SOURCE			
gene			
CDS			

	Query Match	Best Local Similarity	82.3%	Score 463.8	DB 12	Length 801	
	Matches	592	Conservative	0	Mismatches 97	Indels 30	Gaps 4
sig_peptide	1. .66						
mat_peptide	67. .387						
mat_peptide	445. .798						
misc_feature	388. .444						
ORIGIN							
	Query Match	50.5%	Score 463.8	DB 12	Length 801		
	Best Local Similarity	82.3%	Pred. No. 3.9e-119				
	Matches	592	Conservative	0	Mismatches 97	Indels 30	Gaps 4
52	GCTACCGTTGGCGACAGCCGATATTGTGTGAAGCAGTCTCCAGGACCCCTGTCTGTCT	111					
49	GTTTCAGATACCATCTGAGAAATAGTATGACGACAGTCTCCAGCACCCCTGTCTGTCT	108					
112	CCAGGGGAAAGACCAACCCCTCTCTCTGACGGGCGCATGAGAGTGTATGAGACGACTACTTA	171					
109	CCAGGGGAAAGACCAACCCCTCTCTCTGACGGGCGCATGAGAGTGTATGAGAACTA	165					
172	GCTTGATACGACGAAAGCTGGCGAGGCTCCAGGCTCCCTCATCTATGATGATCCACC	231					
166	GCTTGATACGACGAAAGCTGGCGAGGCTCCAGGCTCCCTCATCTATGATGATCCACC	225					
232	AGGGCGACTGGCATGCGACAGAGTTCAGTGGCAGTGGGTCCGGACAGACTTCACTCTC	291					
226	AGGGCGACTGGATACCCAGCGAGTTCAGTGGCAGTGGGTCCGGACAGACTTCACTCTC	285					
232	ACCATCAGTACACTGGAGCTGGAAGATTTCACAGTATTATTCATGACAGATATGATGAGC	351					
286	ACCATCAGACCTGCGACGTCTGGAAGATTTCGCAATTATTACTGTACAGCATATATGAA	345					
352	TCACCTCAGACACTCAGATCACTTTCGGCGGAGGAGACCAAGTGGAGATCAAGCACT	411					
346	TGTTTTGG-----ACGTTGGGCGCAAGGAGCTGGAATCAAACTTAGA	393					
412	GTGGCTGACCATCTGTCTCTGGGGGTGGCGGTTCCGAGGTGGTGGATCAGGTGAGGT	471					
394	GTTGAG-----GCGTTTCAAGGGGAGGTGGCTTCTGGCGTGGCGGATGCTTG-----	442					
472	GGCTCCAGGTGACAGTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCTGGGAGGTCTCCTG	531					
443	----AGCAGGTGACAGTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCTGGGAGGTCTCCTG	498					
532	AGACTCTCTGTGACGCTCTGGATTCCCTTCAAGAGCTTGTGATGACATGGGTCCG	591					
499	AGACTCTCTGTGAGCTCTGGATTCACTTCAAGTGTGATCTTATGACCTGCGTCCG	558					
592	CAGGCTCAGGCGAAGGGGCTGGAGTGGTGGCGATTATCATATATGAGAAAGCACTAA	651					
559	CAGGCTCAGGCGAAGGGGCTGGAGTGGTGGCGATTATCATATATGAGAAAGCACTAA	618					
652	TACTACGCAAGCTCCGTAAGGGCGGATTCACATCTCCAGAGACACTTCCAAAGACAG	711					
619	TATTAAGGTAAGCTCATAGAAAGGGCGCACTCACCATCTCCAGAGCAATTCACAGAACG	678					

Qy 712 GTGATCTPAAAAATGAACAGCCTGAGAACTGAGACAGCGCTGTCTATTACTGTGGAG 770  
Db 679 CTGATTGGAAATGAACAGCCTGAGACAGCCTGTGTATTACTGTGGAG 737

RESULT 6  
BD222938  
LOCUS BD222938 1630 bp DNA linear PAT 17-JUL-2003  
DEFINITION Heteromimibodies.  
ACCESSION BD222938  
VERSION BD222938.1 GI:33032708  
KEYWORDS JP 2002521053-A/32.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 1630)  
AUTHORS Kufer,P., Dreier,T., Baeuerle,P.A., Borschert,K. and Zettl,F.  
TITLE Heteromimibodies  
JOURNAL Patent: JP 2002521053-A 32 16-JUL-2002;  
MICROMET AG

COMMENT OS Homo sapiens (human)  
OS Mus musculus (mouse)  
PN JP 2002521053-A/32  
PD 16-JUL-2002  
PF 28-JUL-1999 JP 2000562401  
PI 28-JUL-1998 EP 98114082.5  
PI PETER KUFER, TORSTEN DREIER, PATRICK A BAEUERLE, KATRIN BORSCHERT,  
PI FLORIAN ZETTL  
PC C12N15/09,A61K35/76,A61K38/00,A61K38/21,A61P35/00,A61P35/02,  
PC C07K19/00,  
PC C12N5/10,C12P21/02,G01N33/53,G01N33/53/(C12N5/10,C12R1:91),  
PC (C12P21/02,C12R1:91),C12N15/00,C12N5/00,A61K37/02,A61K37/66,  
PC (C12N5/00,C12R1:91)  
CC Heteromimibodies  
FH Key  
FT CDS Location/Qualifiers  
1..1630  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Query Match 48.5%; Score 445; DB 6; Length 1630;  
Beet Local Similarity 76.3%; Pred. No. 7.6e-114;  
Matches 620; Conservative 0; Mismatches 145; Indels 48; Gaps 4;

Qy 52 GCTACCGTTGCCAGCGCGGATATTGTGTGACGCGAGTCTCCAGGACCCCTGTTGTCT 111  
Db 78 GCTACAGGTGTACATCTCGAGCTCCAGATGACCCAGTCTCCATCTCCCTGTCTGATCT 137

Qy 112 CCAGGGGAAAGAGCCACCCTCTCTGCAAGGGGCGATGAGAGTGTAGTAGAGCGTACTTA 171  
Db 138 GTAGAGACAGAGTACCATCTCTGCGGGGCAAGTCAGAG---CATTAGAGCGCTATTTA 194

Qy 172 GCGTGTACAGCAGCAAAACCTGGCCAGGCTCCAGGCTCTCATCTATGATGATGATCACC 231  
Db 195 AATTGTATCAGCAAAACAGAGCAGGCTCTTAAGTGTCTATTATCGGGCACTTACC 254

Qy 232 AGGGCACTGGCATGCCAGACAGGTTCTAGTGGCAATGGGTCCGGAGACAGACTTCACTTC 291  
Db 255 CGGGAAATCGGGGTCCTGACCGATTGACGGCGCATGTGATCTGGGCAAAATTACACTCTC 314

Qy 292 ACCATCAGTACGAGCTGAGAGCTGAAGATTGTCAGTGTATTACTGTGAGAGATGTATGAC 351  
Db 315 ACCATCAGAGCTGAGAGCTGAGAGATTTTGTCTACTTCTTTGTCAACAGTCTGACAGT 374

Qy 352 TCACCTGACAGACCTCAGATCACTTTGGCGGAGGAGCAAGTGGAGATCAAGCAACT 411  
Db 375 TTGGC-----GATCAGCTTGGCGCAAGGAGACAGCACTGAGACTTCAA----- 416

Qy 412 GTGCTGACACATCTGTCTGTGGCGGTGCGGTTCCGAGAGTGGATCAGTGGAGGT 471  
Db 417 -----GGAGAGAGAGATCAGGTGGTGGTGGTACCGCGCGGC 455

Qy 472 GGCCTCCAGAGTGCAGCTGGTGGAGTCTGGGGAGGCGGTGTCACGCTGGAGGTCCCTG 531  
Db 456 GGCCTCAGAGGTGCAGCTGTGTCAGTCTGGGGAGGCGGTGTCTCAGCTGGAGGTCCCTG 515

Qy 532 AGACTCTCTGTGACAGCTCTGAGATTCCCTTCAGAGAGCTTTGATGACATGGGTCCGC 591  
Db 516 AGACTCTCTGTGACAGCTCTGAGATTCACTTCACTAGCTATGGCATGCACTGGGTCCGC 575

Qy 592 CAGGCTCAGGCAAGGGGCTGAGAGGGGTGAGAGTATATCATATGATGAGCACTAA 651  
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Qy 652 TACTACGAGAGTCCGTTGAGAGGCGGATTCACATCTCCAGAGACATTCAGAGACAG 711  
Db 636 TACTATGAGAGTCCGTTGAGAGGCGGATTCACATCTCCAGAGACATTCAGAGACAG 695

Qy 712 GTGATCTPAAAAATGAACAGCCTGAGAACTGAGACAGCGCTGTCTATTACTGTGGAGA 771  
Db 696 CTGATCTGCAAAATGAACAGCCTGAGAGCTGAGACAGCGCTGTATTACTGTGGAGAA 755

Qy 772 GATCAGACCTGTTGGGTGACT-----ATGACCACTACTAGCTTTGAGCTGTGGGCG 825  
Db 756 GATATGGGTGGGGGAGGTGCTGAGAGCCCTACTACTACTAGATGAGCGTGTGGGCG 815

Qy 826 AAAGGACACAGCGTCAAGCTCTCTCAGAGATCC 858  
Db 816 CAGGAGACACAGCGTCAAGCTCTCTCAGAGATCC 848

RESULT 7  
BD222939  
LOCUS BD222939 1630 bp DNA linear PAT 17-JUL-2003  
DEFINITION Heteromimibodies.  
ACCESSION BD222939  
VERSION BD222939.1 GI:33032709  
KEYWORDS JP 2002521053-A/33.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 1630)  
AUTHORS Kufer,P., Dreier,T., Baeuerle,P.A., Borschert,K. and Zettl,F.  
TITLE Heteromimibodies  
JOURNAL Patent: JP 2002521053-A 33 16-JUL-2002;  
MICROMET AG

COMMENT OS Homo sapiens (human)  
OS Mus musculus (mouse)  
PN JP 2002521053-A/33  
PD 16-JUL-2002  
PF 28-JUL-1999 JP 2000562401  
PI 28-JUL-1998 EP 98114082.5  
PI PETER KUFER, TORSTEN DREIER, PATRICK A BAEUERLE, KATRIN BORSCHERT,  
PI FLORIAN ZETTL  
PC C12N15/09,A61K35/76,A61K38/00,A61K38/21,A61P35/00,A61P35/02,  
PC C07K19/00,  
PC C12N5/10,C12P21/02,G01N33/53,G01N33/53/(C12N5/10,C12R1:91),  
PC (C12P21/02,C12R1:91),C12N15/00,C12N5/00,A61K37/02,A61K37/66,  
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CC Heteromimibodies  
FH Key  
FT CDS Location/Qualifiers  
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/db\_xref="taxon:9606"

ORIGIN

Query Match	48.5%;	Score 445;	DB 6;	Length 1630;
Best Local Similarity	76.3%;	Pred. No. 7,6e-114;		
Matches 620;	Conservative 0;	Mismatches 145;	Indels 48;	Gaps 4;
QY	52	GCTACCGTTGCCACGAGCCGATATTGTTGTAAGCAGTCTCCAGGACCCCTGCTTTGCT	111	
Db	78	GCTACGAGTGTACACTCCGAGCTCCAGATGACCAGTCTCCATCTCTCCCTCTGTGCACT	137	
QY	112	CCAGGGGAAAAGGCCACCTCTTCTGCGAGGGCCAGTCAGAGTGTATGATGACGTA	171	
Db	138	GTAGAGACAGAGTCAACCATCACTTGCCGGGCAAGTCAGAG---CATTAGCAGCTATT	194	
QY	172	GCCTGGTACACACAGAAACCTGACCAGGCTCCAGGCTTCATCTATGAGTCATCCAC	231	
Db	195	AATTGGTATCAGACGAAACACAGACGCTCTTAAGCTGCTATTATCGGGACATCAC	254	
QY	232	AGGGCCACTGGCATGCGACACAGGTTCACTGGCAGTGGGTCCGGACACACTTCACT	291	
Db	255	CGGGAATCCGGGGTCCCTGACCGATTACGCGGACAGTGAATCGGACAATTA	314	
QY	292	ACCATCAGTAGACTGAGCGCTTAAATTTTGAAGTATTAATCTGACAGATATGATG	351	
Db	315	ACCATCAGAGCTGAGCTGAGCTGAATAATTTTGTACTTACTTTTGTCAACAGCTG	374	
QY	352	TCACCTCAGACACTCAGATCACTTTCGGCGAGGAGCAAGAGTGGATCAAA	411	
Db	375	TTGGC-----GATCACCTTCGGCCAAAGGACACGACTGGAATTC	416	
QY	412	GTGGCTGCACATCTGTCTCTGCGCGGTGCGGCTTCGAGGTGTGATCAGTGGAG	471	
Db	417	-----GGAGAGAGAGATACAGTGTGTGTGTGATGCGCGCGCGC	455	
QY	472	GGCTCCAGAGTACAGCTGATGAGTCTGAGGAGAGCGTGTCCAGCTGGAGAGTCC	531	
Db	456	GGCTCAGAGTGTACAGCTGTGAGTCTGGGAGAGCGTGTGTCCAGCTGGAGAGTCC	515	
QY	532	AGACTCTCCTGTGACGCTCTGAGTATCCCTTCAGAACTTTGCTATGCACTGGGT	591	
Db	516	AGACTCTCCTGTGACGCTCTGAGTATCCCTTCAGTATGCTATGATGCACTGGGT	575	
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Db	576	CAGGCTCAGGAAAGGGGCTGAGTGGGTGCGAGTATATGATATGAGAAAGTATTA	635	
QY	652	TACTACGCACTCCGTGAGAGGGCCGATTCACATCTCCAGAGCACTTCCAAAGAC	711	
Db	636	TACTATGCACTCCGTGAGAGGGCCGATTCACATCTCCAGAGCAATTCAAAGAC	695	
QY	712	GTTATCTTAAAAATGAACAGCTTGAACTGAGACAGCGCTGTCTATTA	771	
Db	696	CTGTATCTGCAAAATGAACAGCTTGAGACTGAGACAGCGCTGTGTATTA	755	
QY	772	GATCAGAGCTGTTGGTGTGACT-----ATGACCACTACCTACGGTTTGAAGTCC	825	
Db	756	GATATGGGGTGGGAGAGTGGCTGAGAGACCTCATCTATCTACGGTATGAGAGTCT	815	
QY	826	AAAGGACCAACGCTACCGCTCTCTCAGAGATCC	858	
Db	816	CAAGGACCAACGCTACCGCTCTCTCAGAGATCC	848	
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LOCUS	AX023365	1630 bp	DNA	linear
DEFINITION	Sequence 36 from Patent WO00060605.			
ACCESSION	AX023365			
VERSION	AX023365.1	GI:10183777		
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
REFERENCE	1			

```

AUTHORS      Kufner, P., Zettl, F., Dreier, T., Baenerle, P. A. and Borschert, K.
TITLE        Heterocminibodies
JOURNAL      Patent: WO 0006605-A 36 10-FEB-2000;
              KUFER PETER (DE) ; ZETTL FLORIAN (DE) ; DREIER TORSTEN (DE) ;
              BAENERLE PATRICK A (DE) ; BORSCHERT KATRIN (DE) ; MICRONET GES
              BIOMEDIZINIS (DE)
FEATURES     Location/Qualifiers
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              LSCASGPTFSSYGMHNVROAPGKGLAEWVAIVISYDSNKKYADSVKGRFLIISDNKSN
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              LQSGAGYLSLSVTVPESSSLGQTQTYICNNHKKPSNKKVKKVPEKSCDKRSGGGGSGAP
              ARSSGSPSTQPMWENVALIQEARLLINISRDTPAAMENATVEVISEMFDLQEPYCQTULE
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Query Match	48.5%	Score 445;	DB 6;	Length 1630;
Best Local Similarity	76.3%	Pred. No. 7.6e-114;		
Matches 620; Conservative	0;	Mismatches 145;	Indels 48;	Gaps 4;

[illegible]

Db	255	CGGGATTCGGGGGTCCTCGACCGATTACGCGGAGTGATTTGGACAAATTACACTTC	314
Qy	292	ACCATCAGTAACTGAGGCTGGAAGATTGTCAGTGTATTACTGTGACAGTATGTAGC	351
Db	315	ACCATCAGCAGCCTGACGCTGGAAGATTGTCATTAATTGTCTCAACAGTCTGACAGT	374
Qy	352	TCACCTCAGACCACTCAGATCACTTTGGCGGAGGAGCAAGGTGAGATCAACGAAC	411
Db	375	TTGGC-----GATCACCTTGGCCCAAGGAGACAGACTGGACATTCMA-----	416
Qy	412	GTGGGTGACCATCTGTCTCTGGGGGTGGCGGCTCCGAGGTGGTGGATTCAGGTGAGGT	471
Db	417	-----GGAGAGAGAGAAATCAGGTGGTGGTGGTGGAGCGCGCGGC	455
Qy	472	GGCTCCGAGGTGACAGTGTGGAATCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCTG	531
Db	456	GGCTCAGAGGTGACAGTGTCTGAGATCTGGGGGAGCGGTGGTCCAGCCTGGGAGGTCCTG	515
Qy	532	AGACTCTCTGTGCGAGCCTCTGGAATTCCTCTTCGAAAGCTTTGCTATGACATGGGTCCG	591
Db	516	AGACTCTCTGTGCGAGCCTCTGGAATTCACCTTCAGTAGTATGGACATGACTGGGTCCG	575
Qy	592	CAGCCTCTAGCGCAAGGGGCTGGAATGGGTGGCAGTTATATCATATGATGAAGACATAA	651
Db	576	CAGCCTCAGGCAAGGGGCTGGAATGGGTGGCAGTTATATCATATGATGAAGATATAA	635
Qy	652	TATACGCAAGCTCCGTGAAGGGCCGATTCACCATCTCCAGAGACATTCCAAGACAG	711
Db	636	TACTATGACAGCTCCGTGAAGGGCCGATTCACCATCTCCAGAGACATTCCAAGACAG	695
Qy	712	GTGTATCTAAATGAAAGAGCTGAGACTGAGAGACAGGCTGTCTATTACTGTGCAGA	771
Db	696	CTGTATCTGCAAAATGAAAGAGCTGAGACTGAGAGACAGGCTGTCTATTACTGTGCAGA	755
Qy	772	GATCAGAGCCTGTTGGGTGACT-----ATGACCACTACTACGGTTTGGACGTGTGGGCG	825
Db	756	GATTTGGGGTGGGAGATGGCTGGAGACCCACTACTACTACTACGGTATGAGACGTGTGGGCG	815
Qy	826	AAAGGAGCAACGGTCAACCGTCTCCTCAGAGATCC	858
Db	816	CAGGGAGCAACGGTCAACCGTCTCCTCAGAGATCC	848
RESULT 10			
AF416910			
LOCUS	867 bp	mRNA	linear SYN 22-OCT-2003
DEFINITION	Synthetic construct JB-43 recombinant single chain Fv antibody		
ACCESSION	AF416910		
VERSION	AF416910.1	GI:16033614	
KEYWORDS	.		
SOURCE	synthetic construct		
ORGANISM	synthetic construct		
REFERENCE	1 (bases 1 to 867)		
AUTHORS	Bhatia, Y., Cavill, D., Gordon, T., Planque, S., Taguchi, H.,		
TITLE	Bhatia, G., Nishiyama, Y., Arnett, F. and Paul, S.		
JOURNAL	Vasoactive intestinal peptide binding autoantibodies in autoimmune		
MEDLINE	Peptides 23 (12), 2251-2257 (2002)		
PUBMED	22423999		
REFERENCE	12535706		
AUTHORS	2 (bases 1 to 867)		
TITLE	Bhatia, Y., Li, L., Cavill, D., Gordon, T., Karle, S., Planque, S.,		
JOURNAL	Zhou, Y.-X., Taguchi, H., Bhatia, G., Nishiyama, Y., Arnett, F. and		
MEDLINE	Paul, S.		
PUBMED	Broad distribution and disease association of vasoactive intestinal		
REFERENCE	peptide binding and cleaving autoantibodies		
AUTHORS	Unpublished		
TITLE	3 (bases 1 to 867)		
JOURNAL	Bhatia, Y., Li, L., Cavill, D., Gordon, T., Karle, S., Planque, S.,		
MEDLINE	Zhou, Y.-X., Taguchi, H., Bhatia, G., Nishiyama, Y., Arnett, F. and		
PUBMED	Paul, S.		
REFERENCE	Zhou, Y.-X., Taguchi, H., Bhatia, G., Nishiyama, Y., Arnett, F. and		
AUTHORS	Paul, S.		
TITLE	Broad distribution and disease association of vasoactive intestinal		
JOURNAL	peptide binding and cleaving autoantibodies		
MEDLINE	Unpublished		
PUBMED	3 (bases 1 to 867)		
REFERENCE	Bhatia, Y., Li, L., Cavill, D., Gordon, T., Karle, S., Planque, S.,		
AUTHORS	Zhou, Y.-X., Taguchi, H., Bhatia, G., Nishiyama, Y., Arnett, F. and		
TITLE	Paul, S.		
JOURNAL	Broad distribution and disease association of vasoactive intestinal		
MEDLINE	peptide binding and cleaving autoantibodies		
PUBMED	Unpublished		
REFERENCE	3 (bases 1 to 867)		
AUTHORS	Bhatia, Y., Li, L., Cavill, D., Gordon, T., Karle, S., Planque, S.,		
TITLE	Zhou, Y.-X., Taguchi, H., Bhatia, G., Nishiyama, Y., Arnett, F. and		
JOURNAL	Paul, S.		
MEDLINE	Zhou, Y.-X., Taguchi, H., Bhatia, G., Nishiyama, Y., Arnett, F. and		
PUBMED	Paul, S.		
REFERENCE	Zhou, Y.-X., Taguchi, H., Bhatia, G., Nishiyama, Y., Arnett, F. and		
AUTHORS	Paul, S.		







QY 70 GATATTGTGTGAGCGAGTCTCCAGACACCCTGTTTGTCTCCAGGGGAAAGGCAACC 129  
 DB 1 GACATCCGATGACCCAGTCTCCAGACTCCCTGCTGTGTCTGTGGGCGAGAGGCGCACCC 60  
 QY 130 CTCTCTCGAGGGCCAGTCCAGAGTGT-----AGTAGCACTACTTAGGCC 174  
 DB 61 ATCAATCGAAGTCCAGCCAGAGTGTTTATACAGCTCCCAACATAAGAACTACTTAGCT 120  
 QY 175 TGTATCCAGCAAAACCTGGCCAGGCTCCAGCTCTCTCATCTATGATGATCCAGCAG 234  
 DB 121 TGTATCCAGCAAAACCTGGCCAGGCTCTCTCATCTACTTAGCTGAGCATCTACCCG 180  
 QY 235 GGCACGTGGATGCGACAGGTTCACTGAGTGGATGGGATCCGGGACAACTTCACTTCCAC 294  
 DB 181 GAATCCGGGGTCCCTTACCGATTCAGTGGAGGGGATCTGGGACAAATTCCTCTCCACC 240  
 QY 295 ATCAGTAGACTGGAGCTGGAAGATTTTGCAGTATTAATCTGTCAGCAGTATGGTAGCTCA 354  
 DB 241 ATCAGCAGCTGAGAGCTGAGAGTGTGAGATTTATCTGTACGCAATTTATAG----- 296  
 QY 355 CCTCAGACACTTCAGATCACTTTGGCGGAGGAGCCAAAGGTGAGATCAACGCACTGTG 414  
 DB 297 -----TACTCTCAGCTCACTTTCGGCGAAGGACCAAGTGAATCAAAATCCGAGGG 351  
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 DB 352 TCGACCATTAATCTGAT 402  
 QY 475 TCCAGAGTCCAGCTGAGTGTGAGTGTGGGAGGAGCGGTGTCAGGCTGGAGAGTCCCTGAGA 534  
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 QY 535 CTCTCTGTGACGCTCTGTGAGTTCCTCTTCAAGAGTGTGTCTATATGCACTGGGTCCGCGAG 594  
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 QY 595 GCTTATGAGCAAGGGGTGTGAGTGGTGTGGCAGTATATCATATGATGAGAACTAATATAC 654  
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 QY 655 TAGCAGACTCCGTCGAGAGGCGGATTCACCATCTCCAGAGACACTTCCAAAGAACAGCGTG 714  
 DB 583 TAGCAGACTCCGTCGAGAGGCGGATTCACCATCTCCAGAGACACTTCCAAAGAACAGCGTG 642  
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 DB 703 C-----CTGATATGAGAGCTGTGGGGCAAGGGAGCC 732  
 QY 835 ACCGTACCGTCTCTCTCA 852  
 DB 733 ACCGTACCGTCTCTCTCA 750

RESULT 12  
 AF416909 861 bp mRNA linear SYN 22-OCT-2003  
 LOCUS AF416909  
 DEFINITION Synthetic construct JB-14 recombinant single chain Fv antibody  
 ACCESSION AF416909  
 VERSION AF416909.1 GI:16033611  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 synthetic construct  
 other sequences; artificial sequences.  
 1 (bases 1 to 861)  
 Bangele,Y., Cavill,D., Gordon,T., Planque,S., Taguchi,H.,  
 Bhatic,G., Nishiyama,Y., Arnett,F. and Paul,S.  
 Vasoreactive intestinal peptide binding autoantibodies in autoimmune  
 humans and mice

JOURNAL Peptides 23 (12), 2251-2257 (2002)  
 MEDLINE 22423999  
 PUBMED 12535706  
 REFERENCE 2 (bases 1 to 861)  
 AUTHORS Bangele,Y., Li,L., Cavill,D., Gordon,T., Karle,S., Planque,S.,  
 Zhou,Y.-X., Taguchi,H., Bhatic,G., Nishiyama,Y., Arnett,F. and  
 Paul,S.  
 TITLE Broad distribution and disease association of vasoreactive intestinal  
 peptide binding and cleaving autoantibodies  
 JOURNAL Unpublished  
 REFERENCE 3 (bases 1 to 861)  
 AUTHORS Bangele,Y., Li,L., Cavill,D., Gordon,T., Karle,S., Planque,S.,  
 Zhou,Y.-X., Taguchi,H., Bhatic,G., Nishiyama,Y., Arnett,F. and  
 Paul,S.  
 TITLE Direct Submission  
 JOURNAL Submitted (06-SEP-2001) Pathology and Laboratory Medicine,  
 University of Texas-Houston Medical School, 6431 Fannin, Houston,  
 TX 77030, USA  
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 /db\_xref="taxon:9606"  
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 WGIWHPGKGLFEMIGYIVYSGSTVYNSIKRIVTSYDTSKNPSIKLSVTADTA  
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 790..807  
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 817..849  
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 325..372  
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 373..780  
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 Best Local Similarity 71.9%; Pred. No. 1.3e-92;  
 Matches 601; Conservative 0; Mismatches 184; Indels 51; Gaps 7;  
 QY 80 TAGCAGTCTCCAGCACCCTGCTTTGTCTCCAGGGGAAAGGCAACCCTCTCTGCA 139  
 DB 11 TCACGCACTCCACACCCCTGCTTTGTCTCCAGGGGAAAGGCAACCCTCTCTGCA 70  
 QY 140 GGGCAGTCCAGGTGTGTATGACAGCTTACCTGAGTACCAAGCAAGAACTGGCCAG 199  
 DB 71 GGGCAGTCCAGGTGTGTATGACAGCTTACCTGAGTACCAAGCAAGAACTGGCCAG 127  
 QY 200 CTCACAGGCTCTCATGTATGTGATCCACAGGCGCATGGGATGCCAGACAGTTCA 259  
 DB 128 CTCACAGGCTCTCATGTATGTGATCCACAGGCGCATGGGATGCCAGACAGTTCA 187  
 QY 260 GTGGCAGTGGGTCCGGGACAGACTTCACTTCACCATCATGTAGACTGGAGCTGAAGATT 319

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Db      188 GTGGAGTGGTCTGGGACAGACTTCACTTCAACATGACAGACCTGAGCCTGGAAGATT 247
Qy      320 TTGACATGATTAATCTGACAGATATGATGATCTCACTTCAAGACACTGATCACTTTG 379
Db      248 TTGACATTTATTAATCTGACAGACCTGAGCACTGGCTC-----TCACTTTG 295
Qy      380 GCGGAGGAGCAAGGTGAGATCAACGAACGTGTGCTGACCACTGTCTCTGGCGGTG 439
Db      296 GCGGAGGAGCAAGGTGAGATCAACGCTC-----GAGGTGTGAG 337
Qy      440 GGGGTTCCGAGGTGATGATGATGAGGTGGCTCCAGGTGAGCTGTGTGAGATCTG 499
Db      338 GCGGTTCAAGCGAGGTGGCTGTGGCGATGATCACTTCAAGTACAGCTGACAGCTCAG 397
Qy      500 GGGGAGCGGTGTGCTCAAGCTGAGAGTCCCTGAGACTCTCTGTGTGAGCCTCTGATTC 559
Db      398 GCGCAAGACTGTGTGAAGCCTTGGGGACCTGTCCCTCACTGACCTGTCTGTGTGCT 457
Qy      560 CCTTCAGAACTTGTCTATGCACTGGG-----TCCGCAAGCTTGAAGCAAGGGCTGG 613
Db      458 CCATCAGCAGTATGATTAATCTGAGGTGGCTGATCCGCAAGCAAGGAGGAGGCTGG 517
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Db      518 AGTGAGATGGATCATCTATATATACATGAGGAGCACTACTACAACTC--GTCCCTCAAG 574
Qy      674 GCGGATTCACCATCTCCAGAGCACTTCCAAAGCAAGGTATATCTAAATATGAAGGCC 733
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Qy      794 ATGACCACTACTACGCTGCTTGAAGCTCTGGGGCAAGGAGCAAGGCTGACCGTCTCTG 853
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Qy      854 G-----ATCCGAACAAACCTGATCAGCGAAGAGATCTGAACCATCAATCATCAC 903
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RESULT 13
LOCUS   AR139121 450 bp DNA linear PAT 16-JUN-2001
DEFINITION AR139121
ACCESSION AR139121
VERSION   AR139121.1 GI:14481617
KEYWORDS
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 450)
AUTHORS Dan,M.D., Maiti,P.K. and Kaplan,H.A.
TITLES Antigen binding fragments that specifically detect cancer cells,
nucleotides encoding the fragments, and use thereof for the
prophylaxis and detection of cancers
JOURNAL Patent: US 6207153-A 6 27-MAR-2001;
FEATURES
location/Qualifiers
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3.3e-90;
Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      70 GATATTGTGTGACGAGTCTCCAGGACCCCTGTCTTTGTCTCCAGGGAAAGAGCCACC 129
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Qy      130 CTCTCTGAGAGGCCAGTTCAGATGTTATGTAAGACTTATACCTGGTATCCAGAGAAA 189
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Qy      250 GACAGGTTCAAGTGGAGTGGGTCCGAGACAGACTTCACTTCAATCAATGATGATGAG 309
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Qy      310 CTTGAAGATTTTGAAGTATTAATCTGTACAGAGATGATGATGATGATGATGATGAT 369
Db      138 CTTGAAGATTTTGAAGTATTAATCTGTACAGAGATGATGATGATGATGATGATGAT 79
Qy      370 ATCACTTTGGGCGAGGAGCAAGGATGAGATCAACGAACGATGAGTGCACATCTGTC 429
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Db      18 T 18

RESULT 14
LOCUS   AR139120 450 bp DNA linear PAT 16-JUN-2001
DEFINITION AR139120
ACCESSION AR139120
VERSION   AR139120.1 GI:14481616
KEYWORDS
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 450)
AUTHORS Dan,M.D., Maiti,P.K. and Kaplan,H.A.
TITLES Antigen binding fragments that specifically detect cancer cells,
nucleotides encoding the fragments, and use thereof for the
prophylaxis and detection of cancers
JOURNAL Patent: US 6207153-A 4 27-MAR-2001;
FEATURES
location/Qualifiers
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ORIGIN
Query Match 39.2%; Score 359.4; DB 6; Length 450;
Best Local Similarity 99.7%; Pred. No. 9.2e-90;
Matches 360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      250 GACAGGTTCAAGTGGAGTGGGTCCGAGACAGACTTCACTTCAATCAATGATGATGAG 309
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Qy      310 CTTGAAGATTTTGAAGTATTAATCTGTACAGAGATGATGATGATGATGATGATGAT 369
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Db      373 ATCAGCTTGGCGGAGGACCAAGGTGAGATCAACAGACTGTGCTGCACCATCTGTC 432
Qy      430 T 430
Db      433 T 433

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MMUJ5051      790 bp      mRNA      linear      ROD 06-MAY-1998
LOCUS      Mus musculus VSV-IND neutralising scFv antibody fragment generated
DEFINITION      from the germline precursor of antibody V124.
ACCESSION      AJ005051.1 GI:3123634
VERSION      scFv fragment; V124 antibody.
KEYWORDS      Mus musculus (house mouse)
SOURCE      Mus musculus
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE      1
AUTHORS      Kalinke, U. and Lamarre, A.
TITLE      In vitro affinity maturation of VSV-specific single-chain Fv
JOURNAL      antibody fragments
REFERENCE      2 (bases 1 to 790)
AUTHORS      Kalinke, U.
TITLE      Direct Substitution
JOURNAL      Submitted (30-MAR-1998) Kalinke U., Institute of Experimental
Immunology, Department of Pathology, Schmelzbergstr. 12, 8091
Zuerich, SWITZERLAND
COMMENT      Related sequence: X97498.
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Query Match      39.0%; Score 358.4; DB 10; Length 790;
Best Local Similarity 71.6%; Pred. No. 1.8e-89;
Matches 530; Conservative 0; Mismatches 171; Indels 39; Gaps 3;

Qy      70 GATATTGTTGACGACAGTCTCCAGGACCCCTGTCTTGTCTCCAGGGGAAAGACCAACC 129
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Qy      130 CTCTCTGAGGGCCAGTCAAGTGTAGTACAG-----CTACTTAGCC 174
Db      89 ATGAGCTGCAAGTCAAGTCAAGAGCCCTTTATATAGTACCAATCAAAAGAACTACTGGCC 148
Qy      175 TGGTACGACGAAACCTGGGCGAGGCTCCAGGCTCCATCTATGAGTGCATCCACGAG 234
Db      149 TGGTACGACGAAACCGAGGCGAGTCTCTTAACTGCTGATTACTGGGCAATCCACTAGG 208
Qy      235 GCCACTGGCATCCAGACAGTTCAGTGGAGTGGGTCGGGACAGACTTCACTCTCAC 294
Db      209 GAATCTGGGGGTCCCTGATGCTTCAAGGCAATGAGATCGGACAGATTTCACCTCAC 268
Qy      295 ATCAGTAGCTGAGCCTGAAGATTTCAGATGATTAAGTGTACAGAGTATGTTAGTCTCA 354

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Qy      415 GCTGACCAATCTGTCTTGGCGGTGGCGGTTCCGAGAGTGTGATCAAGTGGAGGTGC 474
Db      374 G-----GTGGTTCTGGCGCGCGGCTCCGAGGTGTGATCCGAGGTGAGGT 424
Qy      475 TCCAGGTGACGTGTGAGTCTGGGGGAGCGTGTCCAGCTGGAGAGTCCCTGAG 534
Db      425 TCCAGTGTGACGTGTGAGTCTGGGGGAGCTTAGTGCAGCTGGAGAGTCCGAGAA 484
Qy      535 CTCTCTGTGACGCTCTGATTTCCCTTCAGAACTTTGCTATGACACTGGGTCCGACAG 594
Db      485 CTCTCTGTGACGCTCTGATTTCACTTTCACTTTGGAATGCACTGGGTTCGTGAG 544
Qy      595 GCTTAGGCAAGGGGCTGAGTGGGTGGAGTTATATCATATGATGAAAGCACTAAATAC 654
Db      545 GCTCCAGAGAAAGGGGCTGAGTGGGTGGCATATCATTAAGTGGCAGTAGTACCATCTAC 604
Qy      655 TACGAGACTCCGTGAAGGCGCATTCACCAATCCAGAGACACTTCAAGAAACGCTG 714
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Qy      715 TATCTAAATGAACAGCCTGAGAACTGAGACACAGGCTGTCTATTACTGTGCGAGAT 774
Db      665 TTCCGTGAATGACCAAGTCTAAGTCTGAGACACAGGCAATGATATTACTGTGCAAGATG 724
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Search completed: February 18, 2005, 07:22:11  
Job time : 4381 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 18, 2005, 04:03:21 ; Search time 616 Seconds

(without alignments)  
8821.952 Million cell updates/sec

Title: US-09-194-164-13

Perfect score: 918  
Sequence: 1 GAATTCATGAAAAAACCAGC.....ATCACCATTAGTGAAGCTT 918

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_16dec04:\*  
1: geneeqn19808:\*  
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3: geneeqn20008:\*  
4: geneeqn20018:\*  
5: geneeqn20028:\*  
6: geneeqn20038:\*  
7: geneeqn20048:\*  
8: geneeqn20058:\*  
9: geneeqn20068:\*  
10: geneeqn20078:\*  
11: geneeqn20088:\*  
12: geneeqn20098:\*  
13: geneeqn20108:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	918	100.0	918	2	AAV10118 Human H11
2	918	100.0	918	4	AAO04537 Human mon
3	918	100.0	918	9	ACA62168 C-antigen
4	918	100.0	918	12	AD052295 Human ant
5	916.4	99.8	918	4	AAO04538 Human H11
6	916.4	99.8	918	12	AD052297 Human ant
7	799.6	87.1	867	2	AAV10119 Human H11
8	799.6	87.1	867	4	AAO04539 Human mon
9	799.6	87.1	867	9	ACA62170 C-antigen
10	799.6	87.1	867	12	AD052298 Human ant
11	798	86.9	867	4	AAO04540 Human H11
12	798	86.9	867	12	AD052300 Human ant
13	457	49.8	1103	12	ADP83553 Anti-teta
14	445	48.5	1630	3	AAZ50588 HD706CFV-
15	445	48.5	1630	3	AAZ50587 HD706CFV-
16	431.2	47.0	756	12	AD058063 S2 cell d
17	395.2	43.1	840	10	ACF58047 HIV-1 neu
18	361	39.3	450	4	AAO04530 Human H11
19	361	39.3	450	12	AD052288 Human ant
20	359.4	39.2	450	2	AAV10111 Human mon

## ALIGNMENTS

21	359.4	39.2	450	4	AAO04529	AAO04529 Human mon
22	359.4	39.2	450	9	ACA62160	ACA62160 Human C-a
23	359.4	39.2	450	12	AD052286	AD052286 Human ant
24	348.4	38.0	762	10	ADH44203	ADH44203 gfv antib
25	346.4	37.7	828	13	ADT02273	ADT02273 Human-lyp
26	345.8	37.7	1574	3	AAZ57599	AAZ57599 Erythrocy
27	345.2	37.6	783	2	AAO08490	AAO08490 Anti-C5 M
28	343.6	37.4	786	10	ADH44205	ADH44205 gfv antib
29	343.6	37.4	1648	2	AAV96346	AAV96346 Chimeric
30	342.8	37.3	771	10	ADH44204	ADH44204 gfv antib
31	337.8	36.8	762	12	AD040403	AD040403 Single ch
32	336.8	36.7	741	12	AD040399	AD040399 Single ch
33	336.8	36.7	756	12	AD040396	AD040396 Single ch
34	336.8	36.7	759	12	AD040397	AD040397 Single ch
35	336.2	36.6	741	13	ADT02275	ADT02275 Human-lyp
36	335.2	36.5	756	12	AD040400	AD040400 Single ch
37	334.6	36.4	1953	9	ACF05482	ACF05482 Anti-CD7
38	334.6	36.4	1956	9	ACF05481	ACF05481 Anti-CD7
39	329	35.8	786	10	ADH44207	ADH44207 gfv antib
40	328	35.7	5227	2	AAV79537	AAV79537 Plasmid p
41	326	35.5	888	5	ACA62158	ACA62158 Human C-a
42	325.4	35.4	543	9	AD052285	AD052285 Human ant
43	325.4	35.4	543	12	AD052283	AD052283 Human ant
44	325.4	35.4	543	12	AD052283	AD052283 Human ant
45	324.4	35.3	543	2	AAV10110	AAV10110 Human mon

RESULT 1  
AAV10118  
ID AAV10118 standard; DNA, 918 BP.

AAV10118;  
29-MAY-1998 (first entry)

Human H11-scFv construct monomer forming DNA sequence.  
H11; monoclonal antibody; Mab; C-antigen; variable region heavy chain;  
V region; H chain; neoplasia; detection; lymphoma; tumor cell; probe;  
primer; vaccine; gene therapy; glioblastoma; neuroblastoma;  
malignant melanoma; adenocarcinoma; small cell lung carcinoma;  
single chain variable region; scFv; ss.  
Synthetic.  
Homo sapiens.

Key Location/Qualifiers  
CDS 1..918  
FT /\*tag= a  
FT /product= "H11-scFv construct"  
FT /note= "partial sequence of monomer forming construct is  
interrupted by an intron."  
FT 907..912  
FT /\*tag= b

intron

WO9744461-A2.

27-NOV-1997.

22-MAY-1997; 97WO-US008962.

22-MAY-1996; 96US-00657449.

(NOVO-) NOVOPHARM BIOTECH INC.

Dan MD, Waitl PK, Kaplan HA;

WPI, 1998-018515/02.  
P-PsDB; AAM40070.

PT Antigen binding fragment from monoclonal antibody, H11 - allows tumour  
 PT specific detection and treatment of neoplasia.

XX Example 7; Page 90-91; 126pp; English.

CC This sequence encodes a human H11 monoclonal antibody single chain V  
 CC region fragment (H11-scFv) construct which is capable of forming  
 CC monomers. This construct is used to determine the ability of H11-scFv  
 CC antibodies to bind specifically to the C-antigen on cancer cells.  
 CC Such antigen binding fragments may be used for treating a patient with  
 CC neoplasia. It is especially useful in the detection of lymphomas and  
 CC leukemias where the tumour cells bearing the C antigen are circulating  
 CC in the patients bloodstream. The polynucleotide sequence may be used as a  
 CC primer or a probe and the encoded protein may be used in a vaccine or for  
 CC gene therapy. The human monoclonal antibody (Mab), designated H11,  
 CC specifically recognises cancerous cells. H11 is specific for  
 CC glioblastoma, neuroblastoma, malignant melanoma, breast adenocarcinoma,  
 CC lung adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and  
 CC prostate adenocarcinoma

XX Sequence 918 BP; 213 A; 240 C; 264 G; 201 T; 0 U; 0 Other;

Query Match 100.0%; Score 918; DB 2; Length 918;

Best Local Similarity 100.0%; Pred. No. 1.8e-227; Mismatches 0; Gaps 0;

Matches 918; Conservative 0; Indels 0; Gaps 0;

QY 1 GAATTCATGAAAAAACCCTATCGCATGCGATGCACTGGCTGGTTGGCTACCGTT 60

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QY 61 GCGCAGGCGCATATGTTGTTGACGCAAGTCCAGGACCCCTGTTGCTCCAGGAGAA 120

DB 61 GCGCAGGCGCATATGTTGTTGACGCAAGTCCAGGACCCCTGTTGCTCCAGGAGAA 120

QY 121 AGAGCAACCTCTCTGCAAGGCGCAGTCAAGTGTAGTAGCACTACTTACCTGGTAC 180

DB 121 AGAGCAACCTCTCTGCAAGGCGCAGTCAAGTGTAGTAGCACTACTTACCTGGTAC 180

QY 181 CACACAAAACTTGGCCAGGCTCCAGGCTCTCATCTATGTTGTCATCCACAGGCTCACT 240

DB 181 CACACAAAACTTGGCCAGGCTCCAGGCTCTCATCTATGTTGTCATCCACAGGCTCACT 240

QY 241 GGCATCCAGACAGTTCAGTGTGAGTGGTCCGGAGACAGACTTCACTCCACATCACT 300

DB 241 GGCATCCAGACAGTTCAGTGTGAGTGGTCCGGAGACAGACTTCACTCCACATCACT 300

QY 301 AGACTGAGGCTGAAAGATTTTTCAGTGTATTTACTGTCAAGCATGTATGATCACTCAG 360

DB 301 AGACTGAGGCTGAAAGATTTTTCAGTGTATTTACTGTCAAGCATGTATGATCACTCAG 360

QY 361 ACACTTCATATCATCTTTCCGCGGAGGACCAAGTGTGAATCAAGAACTGTGGTGTCA 420

DB 361 ACACTTCATATCATCTTTCCGCGGAGGACCAAGTGTGAATCAAGAACTGTGGTGTCA 420

QY 421 CCATCTGTCTTGGCGGTGGCGGTTCCGAGGTGTGATACAGAGTGAAGTGGCTCCAG 480

DB 421 CCATCTGTCTTGGCGGTGGCGGTTCCGAGGTGTGATACAGAGTGAAGTGGCTCCAG 480

QY 481 GTGCAGCTGTGTGAGTCTGGGGGAGGCGTGTTCACGCTTGGAGAGTCCCTGAGACTTCC 540

DB 481 GTGCAGCTGTGTGAGTCTGGGGGAGGCGTGTTCACGCTTGGAGAGTCCCTGAGACTTCC 540

QY 541 TGTGCAAGCTCTGGATTTCCCTTCAGAACTTTGCTATCATCATGCTGGTCCGCAAGGCTCTA 600

DB 541 TGTGCAAGCTCTGGATTTCCCTTCAGAACTTTGCTATCATCATGCTGGTCCGCAAGGCTCTA 600

QY 601 GGCAGAGGCTGTGAGTGTGTGCAATTATCATATGATGAAAGCACTAAATACTACGA 660

DB 601 GGCAGAGGCTGTGAGTGTGTGCAATTATCATATGATGAAAGCACTAAATACTACGA 660

QY 661 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACCTTCCAGAAACGGGTATCTTA 720

DB 661 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACCTTCCAGAAACGGGTATCTTA 720

QY 721 AAAATGAACGCTTGAGAACTGAGACACGCGTGTCTATTACTGTGCGAGATCAGAGC 780

DB 721 AAAATGAACGCTTGAGAACTGAGACACGCGTGTCTATTACTGTGCGAGATCAGAGC 780

QY 781 CTTGTTGGGAGTATGACCACTACCTAGTTTGAACGTCTGGGGCAAGGGGCAACGGTTC 840

DB 781 CTTGTTGGGAGTATGACCACTACCTAGTTTGAACGTCTGGGGCAAGGGGCAACGGTTC 840

QY 841 ACCGTCCTCTCAGATCCGAAACAAAACCTGATCAGCGAAGATCTGAACCATCAGCAT 900

DB 841 ACCGTCCTCTCAGATCCGAAACAAAACCTGATCAGCGAAGATCTGAACCATCAGCAT 900

QY 901 CACCATTTAGTGAAGCTT 918

DB 901 CACCATTTAGTGAAGCTT 918

RESULT 2

AAD04537

ID AAD04537 standard; DNA; 918 BP.

AC AAD04537;

XX 04-JUL-2001 (first entry)

DE Human monoclonal antibody H11-single chain variable region (scFv) DNA #1.

XX Human; monoclonal antibody; Mab; H11; single chain variable region; scFv;

KW neoplastic disease; melanoma; immunoglobulin IGM; gene therapy; lymphoma;

KW carcinoma; breast; lung; gastric; prostate; ovary; colon; lung; vaccine;

KW neuroblastoma; soft tissue sarcoma; prostatic adenocarcinoma; cytostatic;

KW C-antigen; chronic leukemia; glioma; ds.

XX Homo sapiens.

XX Homo

XX Key

XX CDS

XX 1..918

XX /tag= a

XX /product= "Human H11-single chain variable region (scFv)"

XX /transl\_except= (pos:904..915, aa:His-Lys)

XX /note= "Insertion of two inframe stop codon alters the

XX reading frame; CDS does not include start and stop

XX /partial

XX /tag= b

XX /note= "Encodes (SGGG) 3 linker sequence"

XX US6207153-B1.

XX 27-MAR-2001.

XX 22-MAY-1997; 97US-00862124.

XX 22-MAY-1996; 96US-00657449.

XX (VIVE-) VIVENTIA BIOTECH INC.

XX Dan MD, Maiti PK, Kaplan HA;

XX MPI: 2001-289584/30.

XX P-PSDB: AAB00947.

XX Composition comprising antigen binding fragments of an antibody that

XX recognizes an antigen on neoplastic cells but not on normal cells for use

XX in diagnosis, imaging and treatment of carcinomas.

XX Example 7; Col 61-64; 56pp; English.

XX The present DNA sequence encodes human monoclonal antibody (Mab), H11-

XX single chain variable region (scFv). The H11 light chain variable region

XX is linked to the heavy chain variable region through a (SGGG) 3 linker to

CC form monomers. The invention relates to human monoclonal antibody (Mab)  
 CC H11, H11-(scFv) single chain variable (V) region fragment and their  
 CC corresponding DNA molecules. H11 antibody is an immunoglobulin of 19M  
 CC subunits which is specific to C-antigen found specifically on neoplastic  
 CC cells and not on normal cells. H11 is an antibody obtained from the  
 CC fusion of peripheral blood lymphocytes of a 64 year old male with a low  
 CC grade glioma and fused to a human myeloma cell line to produce a  
 CC hybridoma designated NB6M1/H11. A pharmaceutical composition comprising  
 CC H11 and its derivatives are useful in the diagnosis, imaging and  
 CC treatment of neoplastic disease, particularly, melanoma, breast  
 CC carcinoma, lung carcinoma, ovarian carcinoma, colon carcinoma, gastric  
 CC carcinoma, prostate carcinoma, lymphoma carcinoma, neuroblastoma, glioma,  
 CC soft tissue sarcoma, small cell lung carcinoma, prostatic adenocarcinoma,  
 CC B and T cell lymphomas and chronic leukaemias. H11 DNA is also used in  
 CC vaccines and gene therapy

XX Sequence 918 BP; 213 A; 240 C; 264 G; 201 T; 0 U; 0 Other;

Query Match 100.0%; Score 918; DB 4; Length 918;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-227;  
 Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 GAATTCATGAAAAAACCCTATCCGATCGCATGTCACCTGCTGTTCCCTACCGTT 60
DB 1 GAATTCATGAAAAAACCCTATCCGATCGCATGTCACCTGCTGTTCCCTACCGTT 60
QY 61 GCGCAGCCGATATTTGTGTTGACGAGTCTCAAGCACCCTGTCTTTGTCTCCAGGGAA 120
DB 61 GCGCAGCCGATATTTGTGTTGACGAGTCTCAAGCACCCTGTCTTTGTCTCCAGGGAA 120
QY 121 AGAGCACCCTCTCTGCGAGGGCCGATCGAGTGTAGTAGAGCACTTACCTGTATC 180
DB 121 AGAGCACCCTCTCTGCGAGGGCCGATCGAGTGTAGTAGAGCACTTACCTGTATC 180
QY 181 CAGCAGAAACCTGCGCAGGCTCCAGGCTCTCATCTATGTGTCATCCACAGGGCACT 240
DB 181 CAGCAGAAACCTGCGCAGGCTCCAGGCTCTCATCTATGTGTCATCCACAGGGCACT 240
QY 241 GGCATGCCAGACAGGTTCACTGAGTGGCAGTGGGTCCGGAGCAGACTTCACTCCATCACT 300
DB 241 GGCATGCCAGACAGGTTCACTGAGTGGCAGTGGGTCCGGAGCAGACTTCACTCCATCACT 300
QY 301 AGACTGGAGCCGTGAAGATTTTGCAGTGTATTACTGTACAGCACTATGTAGTGCACCTCAG 360
DB 301 AGACTGGAGCCGTGAAGATTTTGCAGTGTATTACTGTACAGCACTATGTAGTGCACCTCAG 360
QY 361 ACACCTCAGATCACTTTCGCGCGAGGAGCAAGGTGAGATCAAAAGAACTGTGGCTGCA 420
DB 361 ACACCTCAGATCACTTTCGCGCGAGGAGCAAGGTGAGATCAAAAGAACTGTGGCTGCA 420
QY 421 CCATCTGTCTCTGCGCGTGGCGGTTCCGAGGTTGATCAGGTGAGAGTGGCTCCGAG 480
DB 421 CCATCTGTCTCTGCGCGTGGCGGTTCCGAGGTTGATCAGGTGAGAGTGGCTCCGAG 480
QY 481 GTGCGAGTGTGAGATCTGCGGGAGGCGGTGTCCAGCCCTGGAGAGTCCCTGAGACTCTCC 540
DB 481 GTGCGAGTGTGAGATCTGCGGGAGGCGGTGTCCAGCCCTGGAGAGTCCCTGAGACTCTCC 540
QY 541 TGTGAGCCTCTGAGATTCCTCTTCAAGACTTGTGATGCACTGGGTCCGACGGCTCTA 600
DB 541 TGTGAGCCTCTGAGATTCCTCTTCAAGACTTGTGATGCACTGGGTCCGACGGCTCTA 600
QY 601 GGCAGAGGAGCTGAGATGAGTGGAGTATATCATATGATGAGAAAGCACTAAATATCAGCA 660
DB 601 GGCAGAGGAGCTGAGATGAGTGGAGTATATCATATGATGAGAAAGCACTAAATATCAGCA 660
QY 661 GACTCCGTTGAAGGGCCGATTCACTTCACAGACACTTCCAAAGAACCGGTATATCTA 720
DB 661 GACTCCGTTGAAGGGCCGATTCACTTCACAGACACTTCCAAAGAACCGGTATATCTA 720
QY 721 AAAATGAACAGCCTGAGAACTGAGACAACGCTGTCTATTACTGTGCGAGAGATCAGAGC 780
DB 721 AAAATGAACAGCCTGAGAACTGAGACAACGCTGTCTATTACTGTGCGAGAGATCAGAGC 780

```

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QY 781 CTGTTGGTGACTATGACCACTACTACGCTTTGACGCTTGGGGCAAGGACCAAGCTC 840
DB 781 CTGTTGGTGACTATGACCACTACTACGCTTTGACGCTTGGGGCAAGGACCAAGCTC 840
QY 841 ACCGCTCTCCTCGAGATCCGACAAAGATGATCAGAGAGATCTGAACCATCAGCAT 900
DB 841 ACCGCTCTCCTCGAGATCCGACAAAGATGATCAGAGAGATCTGAACCATCAGCAT 900
QY 901 CACCATTTAGTGAAGCTT 918
DB 901 CACCATTTAGTGAAGCTT 918

```

# RESULT 3

ACA62168  
 ID ACA62168 strand; DNA; 918 BP.

ACA62168;

07-AUG-2003 (first entry)

C-antigen antibody H11 single chain variable region fragment #1 DNA.

Human; ds; gene; H11; single chain variable region; gene therapy; scFv;  
 neoplasia; tumour; recurrence risk; C-antigen; melanoma; neuroblastoma;  
 glioma; soft tissue sarcoma; small cell lung carcinoma; brain cancer;  
 C-antigen specific antibody; alphac; vaccine; cancer.

Homo sapiens.

Synthetic.

Key Location/Qualifiers

FT CDS 1..918  
 FT /tag= a  
 FT /partial  
 FT /product= "H11 single chain variable region fragment #1"  
 FT /transl\_except= (pos:904..915,aa:His-Lys)  
 FT /note= "No start or stop codon given"

US2003021779-A1.

30-JAN-2003.

13-FEB-2001; 2001US-00782397.

22-MAY-1996; 96US-00657449.

22-MAY-1997; 97US-00862124.

(DANM/) DAN M D.  
 (MAIT/) MAITI P K.  
 (KAPL/) KAPLAN H A.

Dan MD, Maith PK, Kaplan HA;

WPI; 2003-456278/43.

P-PSDB; AB010486.

Novel antigen binding fragment of monoclonal antibody specific for  
 antigen detected on neoplastic cells, useful for diagnosing or treating  
 cancer, for manufacturing novel reagents and as diagnostic and imaging  
 reagent.

Example 7; Page 32-33; 62pp; English.

The invention relates to a polypeptide which is an antigen binding  
 fragment of a monoclonal antibody specific for an antigen detected on  
 neoplastic cells. The antigen binding fragment (ABF) is useful for  
 treating a patient with a neoplasia. The individual has a clinically  
 detectable tumour. The method is useful for palliating the neoplasia. The  
 method reduces the risk of recurrence of a clinically detectable tumour.  
 The antigen binding fragment is labelled with a therapeutic moiety such  
 as radioisotopes or immunomodulators. ABF is useful for detecting C-



CC antigen in a sample. The polypeptide is useful for diagnosing, localising  
 CC and/or treating neoplasias, including melanoma, neuroblastoma, glioma,  
 CC soft tissue sarcoma and small cell lung carcinoma. The polypeptide is  
 CC useful for manufacturing novel reagents and for treating and imaging  
 CC brain cancer. ABF is useful as a diagnostic and imaging reagent. The  
 CC composition is useful for eliciting an immune response against neoplasia.  
 CC The polynucleotide is useful in expression systems for the production of  
 CC C-antigen specific antibody, termed H11 or alphac, as hybridisation  
 CC probes to assay for the presence of alphac polynucleotide or related  
 CC sequences in a sample, as primers to effect amplification of desired  
 CC polynucleotides and in pharmaceutical compositions including vaccines and  
 CC for gene therapy. The polynucleotide is also useful for genetically  
 CC altering cells in vivo, thus treating various types of cancer. The  
 CC polypeptide, polynucleotide and the composition are useful for detecting  
 CC or treating cancer, including therapy of cancer and prophylactic care,  
 CC particularly for decreasing the risk of recurrence. The present sequence  
 CC represents the human C-antigen specific antibody H11 single chain  
 CC variable region fragment, scFv, #1 DNA

XX Sequence 918 BP; 213 A; 240 C; 264 G; 201 T; 0 U; 0 Other;

Query Match 100.0%; Score 918; DB 9; Length 918;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-227;  
 Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCATGAAAAAACCCGCTATCCGAGTCGACGTTCGCTGGTTCGCTACCGTT 60  
 DB 1 GAATTCATGAAAAAACCCGCTATCCGAGTCGACGTTCGCTGGTTCGCTACCGTT 60  
 QY 61 GCGCAGCGCGATTTGTGTGACGCGAGTCTCCAGGACCCCTGCTTGTCTCCAGGGGAA 120  
 DB 61 GCGCAGCGCGATTTGTGTGACGCGAGTCTCCAGGACCCCTGCTTGTCTCCAGGGGAA 120  
 QY 121 AAGACCACTCTCTCTGCGAGGGCAGTCAAGTGTGTAAGTCACTTACCTGCTGAC 180  
 DB 121 AAGACCACTCTCTCTGCGAGGGCAGTCAAGTGTGTAAGTCACTTACCTGCTGAC 180  
 QY 181 CAGCAAAACCTGGCCAGGCTCCAGGCTCCATCATATGTCGATCCACAGGGCACT 240  
 DB 181 CAGCAAAACCTGGCCAGGCTCCAGGCTCCATCATATGTCGATCCACAGGGCACT 240  
 QY 241 GGCATCCAGACAGTTCAGTGGTCCGAGGACAGACTTCACTCTCACTCACTCACT 300  
 DB 241 GGCATCCAGACAGTTCAGTGGTCCGAGGACAGACTTCACTCTCACTCACTCACT 300  
 QY 301 AAGCTGAGCCTGGAAGATTTTGCAGTGTATTAATCTGACAGTATGTAAGTCACTCAG 360  
 DB 301 AAGCTGAGCCTGGAAGATTTTGCAGTGTATTAATCTGACAGTATGTAAGTCACTCAG 360  
 QY 361 ACACCTCAGATCACTTCCGCGGAGGACCAAGGTGAGATCAAAAGAACTGTGGTGA 420  
 DB 361 ACACCTCAGATCACTTCCGCGGAGGACCAAGGTGAGATCAAAAGAACTGTGGTGA 420  
 QY 421 CCATCTGTCTGCGCGGTGGCGTTCCGAGGTGTGTGATCAAGTGGAGTGGTCCGAG 480  
 DB 421 CCATCTGTCTGCGCGGTGGCGTTCCGAGGTGTGTGATCAAGTGGAGTGGTCCGAG 480  
 QY 481 GTGCACTGTGAGATCTGGGGGAGCGGTGTCACGCTGGAGAGTCCCTGAGACTCTCC 540  
 DB 481 GTGCACTGTGAGATCTGGGGGAGCGGTGTCACGCTGGAGAGTCCCTGAGACTCTCC 540  
 QY 541 TGTGCACTGTGAGATCCCTTCAGAACTTTGCTATCACTCGGATCCGCAAGGCTCTA 600  
 DB 541 TGTGCACTGTGAGATCCCTTCAGAACTTTGCTATCACTCGGATCCGCAAGGCTCTA 600  
 QY 601 GGCAGAGGCGCTGAGTGGTGGCAGTTATATCATATGATGAAGCACTAATACTACGCA 660  
 DB 601 GGCAGAGGCGCTGAGTGGTGGCAGTTATATCATATGATGAAGCACTAATACTACGCA 660  
 QY 661 GACTCCGTGAAGGCGGATTCACATCTCCAGAGACACTTCCAGAAACGGGTATCTTA 720  
 DB 661 GACTCCGTGAAGGCGGATTCACATCTCCAGAGACACTTCCAGAAACGGGTATCTTA 720

QY 721 AAATGAACAGCCTGAGAACCTGAGGACACGGCTGTCTTACTGTGCGAGATCAGAGC 780  
 DB 721 AAATGAACAGCCTGAGAACCTGAGGACACGGCTGTCTTACTGTGCGAGATCAGAGC 780  
 QY 781 CTGTTGGGTGACTATAGACCACTACGAGTTTGAAGTCTGGGCGAAAGGACACGCTC 840  
 DB 781 CTGTTGGGTGACTATAGACCACTACGAGTTTGAAGTCTGGGCGAAAGGACACGCTC 840  
 QY 841 ACCGTCCTCTCAGATCCGAAACAACTGATCAGCGAAGAAATCTGAACCATCACT 900  
 DB 841 ACCGTCCTCTCAGATCCGAAACAACTGATCAGCGAAGAAATCTGAACCATCACT 900  
 QY 901 CACCATTTAGTGAAGCTT 918  
 DB 901 CACCATTTAGTGAAGCTT 918

RESULT 4  
 ADOS2295  
 ID ADOS2295 standard; DNA; 918 BP.  
 AC ADOS2295;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX

DE Human antibody H11 scFv DNA #1.  
 XX  
 KW Antigen binding fragment; H chain V region; L chain V region; C-antigen;  
 KW neoplasia; cancer; vaccine; gene therapy; human;  
 KW single chain V region fragment; scFv; gene; ds.  
 OS Homo sapiens.

XX  
 FH Key Location/Qualifiers  
 FT CDS 1..918  
 FT /tag= a  
 FT /product= "Human antibody H11 scFv protein"  
 FT /transl\_except= (pos:904..915, aa:Hls-Lys)  
 FT /partial  
 FT /note= "No start and stop codon"

XX US2004091484-A1.  
 XX  
 PD 13-MAY-2004.

XX 29-AUG-2003; 2003US-00651453.  
 XX  
 PF 22-MAY-1996; 96US-00657449.  
 PR 22-MAY-1997; 97US-00862124.  
 PR 13-FEB-2001; 2001US-00782397.

XX (DANM/) DAN M D.  
 PA (MAIT/) MAITI P K.  
 PA (KAPL/) KAPLAN H A.  
 PA (GRAD/) GRAD C.

PI Dan MD, Maici PK, Kaplan HA, Grad C;  
 XX  
 XX WPI; 2004-399136/37.  
 DR P-PSDB; ADOS2296.  
 XX

PT Composition useful for treating neoplasia in patient, comprises antigen  
 PT binding fragment of antibody specifically recognizing C-antigen  
 PT recognized by antibody comprising H chain V region and L chain V region.  
 XX  
 XX Example 7; SEQ ID NO 13; 56bp; English.

XX The invention relates to a composition comprising an antigen binding  
 CC fragment of an antibody comprising H chain V region and L chain V region  
 CC that specifically recognises C-antigen. The invention is useful for  
 CC treating a patient with a neoplasia. The antigen binding fragment of the  
 CC antibody is used as diagnostic and imaging reagents. The invention is  
 CC useful for genetically altering cells in vivo, to treat various types of

CC cancer. It is also useful in vaccine and gene therapy. The present  
 CC sequence is human antibody H11 single chain V region fragment (scFv) DNA.  
 XX  
 SQ Sequence 918 BP; 213 A; 240 C; 264 G; 201 T; 0 U; 0 Other;

Query Match 100.0%; Score 918; DB 12; Length 918;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-227;  
 Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GAATTCATGAAAAAACCCTATCCGATTCGCGATTGCGACTGGCTGGTTCCGTACCGTT 60
DB 1 GAATTCATGAAAAAACCCTATCCGATTCGCGATTGCGACTGGCTGGTTCCGTACCGTT 60
QY 61 GCGCAGGCCGATATTGTGTGAACGAGTCCAGGCAACCTGCTCTTGTCTCCAGGGGAA 120
DB 61 GCGCAGGCCGATATTGTGTGAACGAGTCCAGGCAACCTGCTCTTGTCTCCAGGGGAA 120
QY 121 AGAGCCACCCCTCTCTGCAAGGCGCAGTCAAGTGTAGTACAGCTACTTACCTGGTAC 180
DB 121 AGAGCCACCCCTCTCTGCAAGGCGCAGTCAAGTGTAGTACAGCTACTTACCTGGTAC 180
QY 181 CAGCAGAAACCTGGCCAGGCTCCAGGCTCTCATCTATGTGATCCACAGGCGCACT 240
DB 181 CAGCAGAAACCTGGCCAGGCTCCAGGCTCTCATCTATGTGATCCACAGGCGCACT 240
QY 241 GGCATGCCAGAGGTTCAAGTGGGTCGCGGACAGACTTCACTCACTCACTCACT 300
DB 241 GGCATGCCAGAGGTTCAAGTGGGTCGCGGACAGACTTCACTCACTCACTCACTCACT 300
QY 301 AGACTGAGACCTGAGATTGTCAGTGTATTAAGTCAAGATGATGATGATGATGATGAT 360
DB 301 AGACTGAGACCTGAGATTGTCAGTGTATTAAGTCAAGATGATGATGATGATGATGAT 360
QY 361 ACACCTCAGATCACTTTCGCGGAGGAGCAAGTGGAGATCAAAAGCACTGTGCTGCA 420
DB 361 ACACCTCAGATCACTTTCGCGGAGGAGCAAGTGGAGATCAAAAGCACTGTGCTGCA 420
QY 421 CCATCTGTCTCGGCGGTGGCGGTCCTCGGAGTGTGATCAAGTGGAGTGGTCCGAG 480
DB 421 CCATCTGTCTCGGCGGTGGCGGTCCTCGGAGTGTGATCAAGTGGAGTGGTCCGAG 480
QY 481 GTGCACTGTGTGAGTCTGGGGGAGCGTGTTCAGGCTGGGAGGTCCTGAGACTCTCC 540
DB 481 GTGCACTGTGTGAGTCTGGGGGAGCGTGTTCAGGCTGGGAGGTCCTGAGACTCTCC 540
QY 541 TGTGCAAGCTCTGATTCCTCTTCAAGACCTTGTGATGCACTGGGTCCGAGGCTCTA 600
DB 541 TGTGCAAGCTCTGATTCCTCTTCAAGACCTTGTGATGCACTGGGTCCGAGGCTCTA 600
QY 601 GGCAGAGGCTGTGAGTGGTGGCAGTATATCATATGATGAGAACCTAAATATCAACGA 660
DB 601 GGCAGAGGCTGTGAGTGGTGGCAGTATATCATATGATGAGAACCTAAATATCAACGA 660
QY 661 GACTCCGTGAAGGGCGGATTCACATCTCCAGAGCACTTCCAGAGCAAGCTGTATCTA 720
DB 661 GACTCCGTGAAGGGCGGATTCACATCTCCAGAGCACTTCCAGAGCAAGCTGTATCTA 720
QY 721 AAATGAAACAGCTGAGAACTGAGAACAGGCTGTCTATTAATCTGTGCGAGATGAGAC 780
DB 721 AAATGAAACAGCTGAGAACTGAGAACAGGCTGTCTATTAATCTGTGCGAGATGAGAC 780
QY 781 CTGTGGGTGATTAAGCACTAATCGGTTTGAAGCTGTGGGGCAAGAGGACCAAGGTC 840
DB 781 CTGTGGGTGATTAAGCACTAATCGGTTTGAAGCTGTGGGGCAAGAGGACCAAGGTC 840
QY 841 ACCGCTCCTCAGATTCGGAACAAAACCTGATCAGGAGAAAGATCTGAACATCAAT 900
DB 841 ACCGCTCCTCAGATTCGGAACAAAACCTGATCAGGAGAAAGATCTGAACATCAAT 900
QY 901 CACCATTAAGTAAAGCTT 918
DB 901 CACCATTAAGTAAAGCTT 918
  
```

RESULT 5  
 AAD04538/C  
 ID AAD04538 standard; DNA; 918 BP.

AC AAD04538;  
 XX  
 DT 04-UTL-2001 (first entry)

DE Human H11-single chain variable region (scFv) complementary DNA #1.

XX Human; monoclonal antibody; Mab; H11; single chain variable region; scFv;  
 XX neoplastic disease; melanoma; immunoglobulin IGM; gene therapy; lymphoma;  
 KW carcinoma; breast; lung; gastric; prostate; ovary; colon; lung; vaccine;  
 KW neuroblastoma; soft tissue sarcoma; prostatic adenocarcinoma; cytostatic;  
 KW C-antigen; chronic leukemia; glioma; ds.

OS Homo sapiens.

PN US6207153-B1.

PD 27-MAR-2001.

PF 22-MAY-1997; 97US-00862124.

PR 22-MAY-1996; 96US-00657449.

XX (VIVE-) VIVENTIA BIOTECH INC.

PA Dan MD, Maitl PK, Kaplan HA;

DR WPI, 2001-289584/30.

XX Composition comprising antigen binding fragments of an antibody that  
 PT recognizes an antigen on neoplastic cells but not on normal cells for use  
 PT in diagnosis, imaging and treatment of carcinomas.

XX Example 7; Col 65-66; 56pp; English.

XX The present sequence is human monoclonal antibody (Mab), H11-single chain  
 CC variable region (scFv) complementary DNA. The invention relates to human  
 CC monoclonal antibody (Mab) H11, H11-(scFv) single chain variable (V)  
 CC region fragment and their corresponding DNA molecules. H11 antibody is an  
 CC immunoglobulin of IGM subclass which is specific to C-antigen found  
 CC specifically on neoplastic cells and not on normal cells. H11 is an  
 CC antibody obtained from the fusion of peripheral blood lymphocytes of a 64  
 CC year old male with a low grade glioma and fused to a human myeloma cell  
 CC line to produce a hybridoma designated MBGM/H11. A pharmaceutical  
 CC composition comprising H11 and its derivatives are useful in the  
 CC diagnosis, imaging and treatment of neoplastic disease, particularly,  
 CC melanoma, breast carcinoma, lung carcinoma, ovarian carcinoma, colon  
 CC carcinoma, gastric carcinoma, prostate carcinoma, lymphoma carcinoma,  
 CC neuroblastoma, glioma, soft tissue sarcoma, small cell lung carcinoma,  
 CC prostatic adenocarcinoma, B and T cell lymphomas and chronic leukemias.  
 CC H11 DNA is also used in vaccines and gene therapy

XX Sequence 918 BP; 201 A; 265 C; 239 G; 213 T; 0 U; 0 Other;

Query Match 99.8%; Score 916.4; DB 4; Length 918;  
 Best Local Similarity 99.8%; Pred. No. 4.6e-227;  
 Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 GAATTCATGAAAAAACCCTATCCGATTCGCGATTGCGACTGGCTGGTTCCGTACCGTT 60
DB 1 GAATTCATGAAAAAACCCTATCCGATTCGCGATTGCGACTGGCTGGTTCCGTACCGTT 60
QY 61 GCGCAGGCCGATATTGTGTGAACGAGTCCAGGCAACCTGCTCTTGTCTCCAGGGGAA 120
DB 61 GCGCAGGCCGATATTGTGTGAACGAGTCCAGGCAACCTGCTCTTGTCTCCAGGGGAA 120
QY 121 AGAGCCACCCCTCTCTGCAAGGCGCAGTCAAGTGTAGTACAGCTACTTACCTGGTAC 180
DB 121 AGAGCCACCCCTCTCTGCAAGGCGCAGTCAAGTGTAGTACAGCTACTTACCTGGTAC 180
  
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QY 181 CAGCAGAAACCTGGCCAGGCTCCAGGCTCTCATCTATGTCATCCACAGGCTCACT 240  
DB 738 CAGCAGAAACCTGGCCAGGCTCCAGGCTCTCATCTATGTCATCCACAGGCTCACT 679  
QY 241 GGCATGCCAGACAGTTTCAGTGCAGTGGGTCCGGACAGACTTCACTCTCCACATCACT 300  
DB 678 GGCATGCCAGACAGTTTCAGTGCAGTGGGTCCGGACAGACTTCACTCTCCACATCACT 619  
QY 301 AGACTGAGCCTGGAAGATTTTGAGTGTATTACTGTCAAGATGATGATCACTCCAG 360  
DB 618 AGACTGAGCCTGGAAGATTTTGAGTGTATTACTGTCAAGATGATGATCACTCCAG 559  
QY 361 ACACCTCAGATCACTTTCCGCGAGGACCAAGGTGAGATCAAACTGTGGCTGCA 420  
DB 558 ACACCTCAGATCACTTTCCGCGAGGACCAAGGTGAGATCAAACTGTGGCTGCA 499  
QY 421 CCATCTGTCTCTGGCGGTGGCGGTCCGAGAGTGTGATCAAGTGGAGGTGGCTCCAG 480  
DB 498 CCATCTGTCTCTGGCGGTGGCGGTCCGAGAGTGTGATCAAGTGGAGGTGGCTCCAG 439  
QY 481 GTGCAGCTGTGAGTCTGGGGAGGCGTGTCCAGCTGGAGTCCCTGAGACTCTCC 540  
DB 438 GTGCAGCTGTGAGTCTGGGGAGGCGTGTCCAGCTGGAGTCCCTGAGACTCTCC 379  
QY 541 TGTGACGCTCTGGATTTCCCTTCAGAACTTTGCTATGCACTGGGTCCGCGCTCTA 600  
DB 378 TGTGACGCTCTGGATTTCCCTTCAGAACTTTGCTATGCACTGGGTCCGCGCTCTA 319  
QY 601 GGCAGAGGCTGAGTGGGTGGAGTATATATATATATATATATATATATATATATATAT 660  
DB 318 GGCAGAGGCTGAGTGGGTGGAGTATATATATATATATATATATATATATATATATAT 259  
QY 661 GACTCCGTGAAGGCGGATTCACATCTCCAGAGACATTCACAGAACAGGCTGATCTA 720  
DB 258 GACTCCGTGAAGGCGGATTCACATCTCCAGAGACATTCACAGAACAGGCTGATCTA 199  
QY 721 AAAATGAACAGCTTGAACTGAGACAGGCTGTCTATTACTGTGAGAGATCAGAGC 780  
DB 198 AAAATGAACAGCTTGAACTGAGACAGGCTGTCTATTACTGTGAGAGATCAGAGC 139  
QY 781 CTTGTGGTGAATATGACCACTACTACGTTTGGAGTCTGGGGCAAGGAGCACGGTTC 840  
DB 138 CTTGTGGTGAATATGACCACTACTACGTTTGGAGTCTGGGGCAAGGAGCACGGTTC 79  
QY 841 ACCGTCTCTCAGAGATCCGAAACAAAATGATCAGGAGAAAGATCTGAACATCAACAT 900  
DB 78 ACCGTCTCTCAGAGATCCGAAACAAAATGATCAGGAGAAAGATCTGAACATCAACAT 19  
QY 901 CACCATTAATGTAAGCTT 918  
DB 18 CACCATTAATGTAAGCTT 1  
RESULT 6  
ID AD052297/c standard; DNA; 918 BP.  
AC AD052297;  
XX  
XX 29-JUL-2004 (first entry)  
XX  
XX Human antibody H11 scFv complementary DNA #1.  
XX  
XX Antigen binding fragment; H chain V region; L chain V region; C-antigen;  
XX neoplasia; cancer; vaccine; gene therapy; human;  
XX single chain V region fragment; scFv; gene; de.  
OS Homo sapiens.  
XX  
XX US2004091484-A1.  
PN  
XX  
XX 13-MAY-2004.

XX 29-AUG-2003; 2003US-00651453.  
PF 22-MAY-1996; 96US-00657449.  
XX  
PR 22-MAY-1997; 97US-00862124.  
PR 13-FEB-2001; 2001US-00782397.  
XX  
PA (DANM/) DAN M D.  
PA (MAIT/) MAITI P K.  
PA (KAPL/) KAPLAN H A.  
PA (GRAD/) GRAD C.  
PI Dan MD, Maith PK, Kaplan HA, Grad C;  
XX  
XX WPI; 2004-399136/37.  
DR  
XX  
XX  
XX Composition useful for treating neoplasia in patient, comprises antigen  
PT binding fragment of antibody specifically recognizing C-antigen  
PT recognized by antibody comprising H chain V region and L chain V region.  
XX  
XX Example 7; SEQ ID NO 15; 56pp; English.  
PS  
XX The invention relates to a composition comprising an antigen binding  
CC fragment of an antibody comprising H chain V region and L chain V region  
CC that specifically recognises C-antigen. The invention is useful for  
CC treating a patient with a neoplasia. The antigen binding fragment of the  
CC antibody is used as diagnostic and imaging reagents. The invention is  
CC useful for genetically altering cells in vivo, to treat various types of  
CC cancer. It is also useful in vaccine and gene therapy. The present  
CC sequence is human antibody H11 single chain V region fragment (scFv)  
CC complementary DNA.  
XX  
SQ Sequence 918 BP; 201 A; 265 C; 239 G; 213 T; 0 U; 0 Other;  
XX  
Query Match 99.8%; Score 916.4; DB 12; Length 918;  
Best Local Similarity 99.9%; Pred. No. 4.6e-227;  
Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GAATTCATGAAAAAACCCTATCCGATCGAGTTCGACTGGCTGCTTCCAGGAGAA 60  
DB 918 GAATTCATGAAAAAACCCTATCCGATCGAGTTCGACTGGCTGCTTCCAGGAGAA 859  
QY 61 GGCAGAGCCGATATGTTGAGACGAGTCTCCAGAGCCTCTTGTCTCCAGGAGAA 120  
DB 858 GGCAGAGCCGATATGTTGAGACGAGTCTCCAGAGCCTCTTGTCTCCAGGAGAA 799  
QY 121 AGAGCACCCTCTCTCGAGGGCCAGTCAAGTGTATGATGACGACTTACCTGTGATC 180  
DB 798 AGAGCACCCTCTCTCGAGGGCCAGTCAAGTGTATGATGACGACTTACCTGTGATC 739  
QY 181 CAGCAGAAACCTGGCCAGGCTCCAGGCTCTCATCTATGTCATCCACAGGCTCACT 240  
DB 738 CAGCAGAAACCTGGCCAGGCTCCAGGCTCTCATCTATGTCATCCACAGGCTCACT 679  
QY 241 GGCATGCCAGACAGTTTCAGTGCAGTGGGTCCGGACAGACTTCACTCTCCACATCACT 300  
DB 678 GGCATGCCAGACAGTTTCAGTGCAGTGGGTCCGGACAGACTTCACTCTCCACATCACT 619  
QY 301 AGACTGAGCCTGGAAGATTTTGAGTGTATTACTGTCAAGATGATGATCACTCCAG 360  
DB 618 AGACTGAGCCTGGAAGATTTTGAGTGTATTACTGTCAAGATGATGATCACTCCAG 559  
QY 361 ACACCTCAGATCACTTTCCGCGAGGACCAAGGTGAGATCAAACTGTGGCTGCA 420  
DB 558 ACACCTCAGATCACTTTCCGCGAGGACCAAGGTGAGATCAAACTGTGGCTGCA 499  
QY 421 CCATCTGTCTCTGGCGGTGGCGGTCCGAGAGTGTGATCAAGTGGAGGTGGCTCCAG 480  
DB 498 CCATCTGTCTCTGGCGGTGGCGGTCCGAGAGTGTGATCAAGTGGAGGTGGCTCCAG 439  
QY 481 GTGCAGCTGTGAGTCTGGGGAGGCGTGTCCAGCTGGAGTCCCTGAGACTCTCC 540  
DB 438 GTGCAGCTGTGAGTCTGGGGAGGCGTGTCCAGCTGGAGTCCCTGAGACTCTCC 379

```

QY 541 TGTGACGCTCTGATTTCCCTTCAAGAGCTTGTATGACATGGGTCGCCAGGCTCTTA 600
DB 378 TGTGACGCTCTGATTTCCCTTCAAGAGCTTGTATGACATGGGTCGCCAGGCTCTTA 319
QY 601 GGCMAAGGGCTGAGTGGGTGGAGTTATATCATATGATGAAGCACTAAATCTACGCA 660
DB 318 GGCMAAGGGCTGAGTGGGTGGAGTTATATCATATGATGAAGCACTAAATCTACGCA 259
QY 661 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACATTTCCAAAGAACGGTGTATCTA 720
DB 258 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACATTTCCAAAGAACGGTGTATCTA 199
QY 721 AAAATGAAGAGCTGAGTGAAGTGAAGACAGGCTGTATATCTGTGCGAGAGATCAGAGC 780
DB 198 AAAATGAAGAGCTGAGTGAAGTGAAGACAGGCTGTATATCTGTGCGAGAGATCAGAGC 139
QY 781 CTGTTGGGTGACTATGACCACTACTACGGTTTGAAGCTGTGGGGCAAGGACCAAGCTC 840
DB 138 CTGTTGGGTGACTATGACCACTACTACGGTTTGAAGCTGTGGGGCAAGGACCAAGCTC 79
QY 841 ACCGTCCTCTCAGAGATCCGAACAAAATCTGATCAGGAAAGAGATCTGAACATCACCA 900
DB 78 ACCGTCCTCTCAGAGATCCGAACAAAATCTGATCAGGAAAGAGATCTGAACATCACCA 19
QY 901 CACCATTTAGTGAAGCTT 918
DB 18 CACCATTTAGTGAAGCTT 1

```

```

RESULT 7
AAV10119
ID AAV10119 standard; DNA; 867 BP.
XX
XX AAV10119;
XX
XX 29-MAY-1998 (first entry)
XX
DE Human H11-scFv construct dimer forming DNA sequence.
XX
XX H11, monoclonal antibody; Mab; C-antigen; variable region heavy chain;
XX V region; H chain; neoplasia; detection; lymphoma; tumor cell; probe;
XX primer; vaccine; gene therapy; glioblastoma; neuroblastoma;
XX malignant melanoma; adenocarcinoma; small cell lung carcinoma;
XX single chain variable region; scFv; ss.
XX
XX Synthetic.
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..867
XX FT /*tag= a
XX FT /product= "H11-scFv construct"
XX FT /note= "partial sequence of dimer forming construct is
XX FT interrupted by an intron."
XX FT 856..861
XX FT /*tag= b
XX
XX WO9744461-A2.
XX
XX 27-NOV-1997.
XX
XX 22-MAY-1997; 97WO-US008962.
XX
XX 22-MAY-1996; 96US-00657449.
XX
XX (NOVO-) NOVOPHARM BIOTECH INC.
XX
XX Dan MD, Malet PK, Kaplan HA;
XX
XX WPI, 1998-018515/02.
XX
XX P-PsDB; AAW40071.
XX

```

PT Antigen binding fragment from monoclonal antibody, H11 - allows tumour  
 PT specific detection and treatment of neoplasia.

PS Example 7; Page 94-95; 126pp; English.

XX This sequence encodes a human H11 monoclonal antibody single chain V  
 CC region fragment (H11-scFv) construct which is capable of forming dimers.  
 CC This construct is used to determine the ability of H11-scFv antibody  
 CC fragments to bind specifically to the C-antigen on cancer cells. Such  
 CC antigen binding fragments may be used for treating a patient with  
 CC neoplasia. It is especially useful in the detection of lymphomas and  
 CC leukemias where the tumour cells bearing the C antigen are circulating  
 CC in the patient's bloodstream. The polynucleotide sequence may be used as a  
 CC primer or a probe and the encoded protein may be used in a vaccine or for  
 CC gene therapy. The human monoclonal antibody (Mab), designated H11,  
 CC specifically recognises cancerous cells. H11 is specific for  
 CC glioblastoma, neuroblastoma, malignant melanoma, breast adenocarcinoma,  
 CC lung adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and  
 CC prostate adenocarcinoma

XX Sequence 867 BP; 209 A; 229 C; 241 G; 188 T; 0 U; 0 Other;

Query Match 87.1%; Score 799.6; DB 2; Length 867;

Best Local Similarity 94.0%; Pred No. 7.9e-197;

Matches 863; Conservative 0; Mismatches 4; Indels 51; Gaps 1;

```

QY 1 GAATTCATGAAAAAAACCGCTATCCGATGAGATTCAGTGGCTGGTTCCGTACCGTT 60
DB 1 GAATTCATGAAAAAAACCGCTATCCGATGAGATTCAGTGGCTGGTTCCGTACCGTT 60
QY 61 GCGCAGGCGGATATGTGTGTGACAGAGTCTCCAGAGCAACCTGTTGTCTCCAGGGAA 120
DB 61 GCGCAGGCGGATATGTGTGTGACAGAGTCTCCAGAGCAACCTGTTGTCTCCAGGGAA 120
QY 121 AGAGCCACCTCTCCTGCGAGGGCGAGTCAGAGTGTAGTGAAGAGCTACTTAAAGCTGTAC 180
DB 121 AGAGCCACCTCTCCTGCGAGGGCGAGTCAGAGTGTAGTGAAGAGCTACTTAAAGCTGTAC 180
QY 181 CAGCAAAAACCTGGCCAGGCTCCAGGCTCTCATCTATGTGTGATCCACAGGGCACT 240
DB 181 CAGCAAAAACCTGGCCAGGCTCCAGGCTCTCATCTATGTGTGATCCACAGGGCACT 240
QY 241 GCGATGCCAGACAGGTTCACTGCGAGTGGGTCCGGGACAGACTTCACTTCACATCACT 300
DB 241 GCGATGCCAGACAGGTTCACTGCGAGTGGGTCCGGGACAGACTTCACTTCACATCACT 300
QY 301 AGACTGAGGCGCTGAGATTTTGCAGTGTATCTGTGACAGTATGTGTGTGTGTGTGTGTGT 360
DB 301 AGACTGAGGCGCTGAGATTTTGCAGTGTATCTGTGACAGTATGTGTGTGTGTGTGTGTGT 360
QY 361 ACACCTCAGATCACTTTGCGCGAGAGGACCAAGTGTGAGATCAAGAGACTGTGCTGCA 420
DB 361 ACACCTCAGATCACTTTGCGCGAGAGGACCAAGTGTGAGATCAAGAGACTGTGCTGCA 420
QY 421 CCATCTGTCTCTGCGGCTGCGGTTCCGAGGTGTGATCAGTGTGAGTGTGCTCCAG 480
DB 421 TC-----CGGACAG 429
QY 481 GTGCAAGCTGTGAGTCTGGGGGAGCGGTGTCAGGCTGGAGAGTCCCTGAGACTCTCC 540
DB 481 GTGCAAGCTGTGAGTCTGGGGGAGCGGTGTCAGGCTGGAGAGTCCCTGAGACTCTCC 540
QY 541 TGTGACGCTCTGATTTCCCTTCAAGAGCTTGTATGACATGGGTCGCCAGGCTCTTA 600
DB 490 TGTGACGCTCTGATTTCCCTTCAAGAGCTTGTATGACATGGGTCGCCAGGCTCTTA 549
QY 601 GGCMAAGGGCTGAGTGGGTGGAGTTATATCATATGATGAAGCACTAAATCTACGCA 660
DB 550 GGCMAAGGGCTGAGTGGGTGGAGTTATATCATATGATGAAGCACTAAATCTACGCA 609
QY 661 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACATTTCCAAAGAACGGTGTATCTA 720
DB 610 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACATTTCCAAAGAACGGTGTATCTA 669

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QY 721 AAAATGAACAGCCTGAGAACTGAGACACGCGCTGTCTATTACTGTGCGAGATCGAGC 780  
 Db 670 AAAATGAACAGCCTGAGAACTGAGACACGCGCTGTCTATTACTGTGCGAGATCGAGC 729  
 QY 781 CTTGTTGGGAGCTATATACCACTTCTCGGTTTGGAGCTCGGGGCAAAAGGACACGGTTC 840  
 Db 730 CTTGTTGGGAGCTATATACCACTTCTCGGTTTGGAGCTCGGGGCAAAAGGACACGGTTC 789  
 QY 841 ACCGTCCTCGAGATCCGAAACAACTGATCAGCGAAGAGATCTGAACCATCCATC 900  
 Db 790 ACCGTCCTCGAGATCCGAAACAACTGATCAGCGAAGAGATCTGAACCATCCATC 849  
 QY 901 CACCATTAAGTGAAGCTT 918  
 Db 850 CACCATTAAGTGAAGCTT 867  
 RESULT 8  
 AAD04539 standard; DNA; 867 BP.  
 XX AAD04539:  
 AC AAD04539:  
 DT 04-JUL-2001 (first entry)  
 XX  
 DE Human monoclonal antibody H11-single chain variable region (scFv) DNA #2.  
 XX  
 KW Human; monoclonal antibody; Mab; H11; single chain variable region; scFv;  
 KW neoplastic disease; melanoma; immunoglobulin Igm; gene therapy; lymphoma;  
 KW carcinoma; breast; lung; gastric; prostate; ovary; colon; lung; vaccine;  
 KW neuroblastoma; soft tissue sarcoma; prostatic adenocarcinoma; cytostatic;  
 KW C-antigen; chronic leukaemia; glioma; ds.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..867  
 FT /tag= a  
 FT /product= "Human H11-single chain variable region (scFv)"  
 FT /transl\_except= (pos:853..864, aa:His-Lys)  
 FT /note= "Insertion of two inframe stop codon alters the  
 FT reading frame; CDS does not include start and stop  
 FT codons"  
 FT /partial  
 XX  
 PN US6207153-B1.  
 PD 27-MAR-2001.  
 XX  
 PF 22-MAY-1997; 97US-00862124.  
 XX  
 PR 22-MAY-1996; 96US-00657449.  
 XX  
 PA (VIVE-) VIVENTIA BIOTECH INC.  
 XX  
 PI Dan MD, Maiti PK, Kaplan HA;  
 DR WPI; 2001-289584/30.  
 DR P-PSDB; AAB00948.  
 PT Composition comprising antigen binding fragments of an antibody that  
 PT recognizes an antigen on neoplastic cells but not on normal cells for use  
 PT in diagnosis, imaging and treatment of carcinomas.  
 XX  
 PS Example 7; Col 67-70; 56bp; English.  
 CC The present DNA sequence encodes human monoclonal antibody (Mab), H11-  
 CC single chain variable region (scFv). The H11 light chain variable region  
 CC is linked to the heavy chain variable region through a (SGGGG)3 linker to  
 CC form dimers. The invention relates to human monoclonal antibody (Mab)  
 CC H11, H11-(scFv) single chain variable (V) region fragment and their  
 CC corresponding DNA molecules. H11 antibody is an immunoglobulin of Igm

CC subclase which is specific to C-antigen found specifically on neoplastic  
 CC cells and not on normal cells. H11 is an antibody obtained from the  
 CC fusion of peripheral blood lymphocytes of a 64 year old male with a low  
 CC grade glioma and fused to a human myeloma cell line to produce a  
 CC hybridoma designated NB6M1/H11. A pharmaceutical composition comprising  
 CC H11 and its derivatives are useful in the diagnosis, imaging and  
 CC treatment of neoplastic disease, particularly, melanoma, breast  
 CC carcinoma, lung carcinoma, ovarian carcinoma, colon carcinoma, gastric  
 CC carcinoma, prostate carcinoma, lymphoma carcinoma, neuroblastoma, glioma,  
 CC soft tissue sarcoma, small cell lung carcinoma, prostatic adenocarcinoma,  
 CC B and T cell lymphomas and chronic leukaemias. H11 DNA is also used in  
 CC vaccines and gene therapy  
 XX  
 SQ Sequence 867 BP; 209 A; 229 C; 241 G; 188 T; 0 U; 0 Other;  
 Query Match 87.1%; Score 799.6; DB 4; Length 867;  
 Best Local Similarity 94.0%; Pred. No. 7.9e-197;  
 Matches 863; Conservative 0; Mismatches 4; Indels 51; Gaps 1;  
 QY 1 GAATTCATGAAAAAACCAGCTATCGGATCGGAGTTGCACTGGAGTTCGCTACCGTT 60  
 Db 1 GAATTCATGAAAAAACCAGCTATCGGATCGGAGTTGCACTGGAGTTCGCTACCGTT 60  
 QY 61 GCGCAGGCCGATATGTTGTTGACGAGTCTCAGAGCACTCTTGTCTCCAGGGAA 120  
 Db 61 GCGCAGGCCGATATGTTGTTGACGAGTCTCAGAGCACTCTTGTCTCCAGGGAA 120  
 QY 121 AGAGCCACCTCTCTCCGACGGGCGACATCAGAGTTAGTAAAGCATAGCTCGGTAC 180  
 Db 121 AGAGCCACCTCTCTCCGACGGGCGACATCAGAGTTAGTAAAGCATAGCTCGGTAC 180  
 QY 181 AGAGCCACCTCTCTCCGACGGGCGACATCAGAGTTAGTAAAGCATAGCTCGGTAC 240  
 Db 181 AGAGCCACCTCTCTCCGACGGGCGACATCAGAGTTAGTAAAGCATAGCTCGGTAC 240  
 QY 241 GGCATCCAGACAGGTTCAAGTGGAGTGGTCCGGGACAGACTTCACTCCACATCAGT 300  
 Db 241 GGCATCCAGACAGGTTCAAGTGGAGTGGTCCGGGACAGACTTCACTCCACATCAGT 300  
 QY 301 AGACTGGAGCTGAAATTTTGGAGTGTATTACTGTACAGATAGTATGACTGCTCAG 360  
 Db 301 AGACTGGAGCTGAAATTTTGGAGTGTATTACTGTACAGATAGTATGACTGCTCAG 360  
 QY 361 ACACCTCAGATCACTTTCGCGGAGGACCAAGTGAAGTCAAGAACTGTGGCTGCA 420  
 Db 361 ACACCTCAGATCACTTTCGCGGAGGACCAAGTGAAGTCAAGAACTGTGGCTGCA 420  
 QY 421 CCATCTGTCTTGGCGGTGGCGGTTCCGAGGTGTGATCAGGTGAGGTGCTCCAG 480  
 Db 421 TC-----CGACAG 429  
 QY 481 GTGCAGCTGTGAGTCTTGGGGAGGCGTGTCCAGCTGGGAGGTCCTGAGACTCTCC 540  
 Db 430 GTGCAGCTGTGAGTCTTGGGGAGGCGTGTCCAGCTGGGAGGTCCTGAGACTCTCC 489  
 QY 541 TGTGACGCTTGGATTTCCCTTCAGAAAGCTTGTATGACTGGGTCCGCGACTCTA 600  
 Db 490 TGTGACGCTTGGATTTCCCTTCAGAAAGCTTGTATGACTGGGTCCGCGACTCTA 549  
 QY 601 GGCAGAGGCTGTGAGTGGTGGAGTTATATATATATATATATATATATATATATAT 660  
 Db 550 GGCAGAGGCTGTGAGTGGTGGAGTTATATATATATATATATATATATATATATAT 609  
 QY 661 GACTCCGTGAAGGCGGATTCACATCTCCAGAGACACTTCCAAAGAACAGGGTATCTA 720  
 Db 610 GACTCCGTGAAGGCGGATTCACATCTCCAGAGACACTTCCAAAGAACAGGGTATCTA 669  
 QY 721 AAAATGAACAGCCTGAGAACTGAGACACGCGCTGTCTATTACTGTGCGAGATCGAGC 780  
 Db 670 AAAATGAACAGCCTGAGAACTGAGACACGCGCTGTCTATTACTGTGCGAGATCGAGC 729  
 QY 781 CTTGTTGGGAGCTATATACCACTTCTCGGTTTGGAGCTCGGGGCAAAAGGACACGGTTC 840

Db 730 CTGTTGGAGTACTGACCACTACTAGCTTTGGAGCTGTGGGCAAGGACGAGTC 789  
QY 841 ACCGTCCTCCAGAGATCCGAAACAACTATATGCGCAAGAAATCTGAACCTACCAT 900  
Db 790 ACCGTCCTCCAGAGATCCGAAACAACTATATGCGCAAGAAATCTGAACCTACCAT 849  
QY 901 CACCATTAGTGAAGCTT 918  
Db 850 CACCATTAGTGAAGCTT 867  
RESULT 9  
ACA62170  
ID ACA62170 standard; DNA; 867 BP.  
XX ACA62170;  
AC 07-AUG-2003 (first entry)  
XX  
DT C-antigen antibody H11 single chain variable region fragment #2 DNA.  
XX  
KW Human; db; gene; H11; single chain variable region; gene therapy; scFv;  
KW neoplasia; tumour; recurrence risk; C-antigen; melanoma; neuroblastoma;  
KW glioma; soft tissue sarcoma; small cell lung carcinoma; brain cancer;  
KW C-antigen specific antibody; alphac; vaccine; cancer.  
XX Homo sapiens.  
OS Synthetic.  
FH Key Location/Qualifiers  
FT 1..867  
FT /tag= a  
FT /partial  
FT /product= "H11 single chain variable region fragment #2"  
FT /transl\_except= (pos:853..834,aa:His-Lys)  
FT /note= "No start or stop codon given"  
XX  
PN US2003021779-A1.  
XX  
PD 30-JAN-2003.  
XX  
PF 13-FEB-2001; 2001US-00782397.  
XX  
PR 22-MAY-1996; 96US-00657449.  
PR 22-MAY-1997; 97US-00862124.  
XX  
PA (DANM/) DAN M D.  
PA (MAIT/) MAITI P K.  
PA (KAPL/) KAPLAN H A.  
XX  
PI Dan MD, Maith PK, Kaplan HA;  
XX  
DR WPI; 2003-456278/43.  
DR P-PsDB; ABU10487.  
XX  
PT Novel antigen binding fragment of monoclonal antibody specific for  
PT antigen detected on neoplastic cells, useful for diagnosing or treating  
PT cancer, for manufacturing novel reagents and as diagnostic and imaging  
PT reagent.  
XX  
PS Example 7; Page 35-36; 62pp; English.  
XX  
CC The invention relates to a polypeptide which is an antigen binding  
CC fragment of a monoclonal antibody specific for an antigen detected on  
CC neoplastic cells. The antigen binding fragment (ABF) is useful for  
CC treating a patient with a neoplasia. The individual has a clinically  
CC detectable tumour. The method is useful for palliating the neoplasia. The  
CC method reduces the risk of recurrence of a clinically detectable tumour.  
CC The antigen binding fragment is labelled with a therapeutic moiety such  
CC as radioisotopes or immunomodulators. ABF is useful for detecting C-  
CC antigen in a sample. The polypeptide is useful for diagnosing, localising  
CC and/or treating neoplasias, including melanoma, neuroblastoma, glioma,  
CC soft tissue sarcoma and small cell lung carcinoma. The polypeptide is

CC useful for manufacturing novel reagents and for treating and imaging  
CC brain cancer. ABF is useful as a diagnostic and imaging reagent. The  
CC composition is useful for eliciting an immune response against neoplasia.  
CC The polynucleotide is useful in expression systems for the production of  
CC C-antigen specific antibody, termed H11 or alphac, as hybridisation  
CC probes to assay for the presence of alphac polynucleotide or related  
CC sequences in a sample, as primers to effect amplification of desired  
CC polynucleotides and in pharmaceutical compositions including vaccines and  
CC for gene therapy. The polynucleotide is also useful for genetically  
CC altering cells in vivo, thus treating various types of cancer. The  
CC polypeptide, polynucleotide and the composition are useful for detecting  
CC or treating cancer, including therapy of cancer and prophylactic care,  
CC particularly for decreasing the risk of recurrence. The present sequence  
CC represents the human C-antigen specific antibody H11 single chain  
CC variable region fragment, scFv, #2 DNA  
XX  
SQ Sequence 867 BP; 209 A; 229 C; 241 G; 188 T; 0 U; 0 Other;  
Query Match 87.1%; Score 799.6; DB 9; Length 867;  
Best Local Similarity 94.0%; Pred. No. 7.9e-197;  
Matches 863; Conservative 0; Mismatches 4; Indels 51; Gaps 1;  
QY 1 GAATTCATGAAAAAACCCTATTCGCGATCGCGAGTTGCACTGCTGCTTCCGAGGAA 120  
Db 1 GAATTCATGAAAAAACCCTATTCGCGATCGCGAGTTGCACTGCTGCTTCCGAGGAA 60  
QY 61 GCGCAGGCGGATATTTGTTGACGAGTCTCCAGGACCCCTGTTGTTCTCCAGGAGAA 120  
Db 61 GCGCAGGCGGATATTTGTTGACGAGTCTCCAGGACCCCTGTTGTTCTCCAGGAGAA 120  
QY 121 AGAGCCACCTCTCTCTCGCGAGGCGCGATCGAGTGTATGACGACTTACCTGCTGAC 180  
Db 121 AGAGCCACCTCTCTCTCGCGAGGCGCGATCGAGTGTATGACGACTTACCTGCTGAC 180  
QY 181 CAGCAAAACCTGGCCAGGCTCCGAGGCTCTCATATGATGATGATGATGATGATGATGAT 240  
Db 181 CAGCAAAACCTGGCCAGGCTCCGAGGCTCTCATATGATGATGATGATGATGATGATGAT 240  
QY 241 GGCATGCCAGACAGGTTGATGAGTGGGATCCGGGACAGACTTCACTGACCATCAGT 300  
Db 241 GGCATGCCAGACAGGTTGATGAGTGGGATCCGGGACAGACTTCACTGACCATCAGT 300  
QY 301 AGACTGGAGCCCTGAAAGATTTTGCAGTGTATTTACTGTCAGCAGTATGATGATGATGAT 360  
Db 301 AGACTGGAGCCCTGAAAGATTTTGCAGTGTATTTACTGTCAGCAGTATGATGATGATGAT 360  
QY 361 ACACCTCAGATCACTTGGCGGAGGACCAAGGTGAGATCAAGAACTGCGGTGCA 420  
Db 361 ACACCTCAGATCACTTGGCGGAGGACCAAGGTGAGATCAAGAACTGCGGTGCA 420  
QY 421 CCATCTGTCTTGGCGGAGGCGGTTCCGAGGTGATGATGATGATGATGATGATGATGAT 480  
Db 421 TC-----CGAACAG 429  
QY 481 GTGCACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540  
Db 481 GTGCACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540  
QY 541 TGTGAGAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600  
Db 541 TGTGAGAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600  
QY 601 GGCAGAGGCGCTGAGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
Db 601 GGCAGAGGCGCTGAGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
QY 661 GACTCTCGTGAAGGCGGATTCACCATCTCCAGAGACATTCGAAAGACGCTGATCTTA 720  
Db 661 GACTCTCGTGAAGGCGGATTCACCATCTCCAGAGACATTCGAAAGACGCTGATCTTA 720  
QY 721 AAAATGAACAGGCTGAGAACGAGGACGAGGCTGATGATGATGATGATGATGATGATGAT 780  
Db 721 AAAATGAACAGGCTGAGAACGAGGACGAGGCTGATGATGATGATGATGATGATGATGAT 780



```
QY 781 CTGTGGGTGACTATGACCACTACTAGCGTTTGACGCTCTGGGGCAAAAGGACCAAGGCTC 840
DB 730 CTGTGGGTGACTATGACCACTACTAGCGTTTGACGCTCTGGGGCAAAAGGACCAAGGCTC 789
QY 841 ACCGTCTCCCTCAGAGATCCGAACAAAACTGATCAGCGAAGATCTGAACTCAATCCAT 900
DB 790 ACCGTCTCCCTCAGAGATCCGAACAAAACTGATCAGCGAAGATCTGAACTCAATCCAT 849
QY 901 CACCATTTAGTGAAGCTT 918
DB 850 CACCATTTAGTGAAGCTT 867

RESULT 10
AD052298
AD052298 standard; DNA; 867 BP.
XX
AC AD052298;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human antibody H11 scFv DNA #2.
XX
KM Antigen binding fragment; H chain V region; L chain V region; C-antigen;
KW neoplasia; cancer; vaccine; gene therapy; human;
XX single chain V region fragment; scFv; gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..867
FT FT /*tag= a
FT FT /product= "Human antibody H11 scFv protein"
FT FT /transl_except= (pos:853..864, aa:His-Lys)
FT FT /partial
FT FT /note= "No start and stop codon"
XX
PN US2004091484-A1.
XX
PD 13-MAY-2004.
XX
PF 29-AUG-2003; 2003US-00651453.
XX
PR 22-MAY-1996; 96US-00657449.
PR 22-MAY-1997; 97US-00862124.
PR 13-FEB-2001; 2001US-00782397.
XX
PA (DANM/) DAN M D.
PA (MAIT/) MAITI P K.
PA (KAPL/) KAPLAN H A.
PA (GRAD/) GRAD C.
XX
PI Dan MD, Maitei PK, Kaplan HA, Grad C;
XX
DR WPI: 2004-399136/37.
DR P-PSDB; AD052298.
XX
PT Composition useful for treating neoplasia in patient, comprises antigen
PT binding fragment of antibody specifically recognizing C-antigen
PT recognized by antibody comprising H chain V region and L chain V region.
XX
XX Example 7; SEQ ID NO 16; 56bp; English.
XX
CC The invention relates to a composition comprising an antigen binding
CC fragment of an antibody comprising H chain V region and L chain V region
CC that specifically recognizes C-antigen. The invention is useful for
CC treating a patient with a neoplasia. The antigen binding fragment of the
CC antibody is used as diagnostic and imaging reagents. The invention is
CC useful for genetically altering cells in vivo, to treat various types of
CC cancer. It is also useful in vaccine and gene therapy. The present
CC sequence is human antibody H11 single chain V region fragment (scFv) DNA.
XX
```

```
SQL Sequence 867 BP; 209 A; 229 C; 241 G; 188 T; 0 U; 0 Other:
Query Match 87.1%; Score 799.6; DB 12; Length 867;
Best Local Similarity 94.0%; Pred. No. 7.9e-197;
Matches 863; Conservative 0; Mismatches 4; Indels 51; Gaps 1;

QY 1 GAATTCAGAAAAAAGCGCTATCCGATCCGAGTTGACCTGGCTTGGCTACCGGT 60
DB 1 GAATTCATGAAAAAAGCGCTATCCGATCCGAGTTGACCTGGCTTGGCTACCGGT 60
QY 61 GCGAGGCGCGATATTGTGTGAAGCAAGTCCAGGACCCCTGTTGTCTCCAGGGAA 120
DB 61 GCGAGGCGCGATATTGTGTGAAGCAAGTCCAGGACCCCTGTTGTCTCCAGGGAA 120
QY 121 AGAGCCACCTCTCTCCGCAAGGCGCAGTCAAGATGTTAAGTACCTTACCTGGTAC 180
DB 121 AGAGCCACCTCTCTCCGCAAGGCGCAGTCAAGATGTTAAGTACCTTACCTGGTAC 180
QY 181 CAGCAAAAACCTGGGCGAGGCTCCGAGGCTCCATCTATGTCATCCACAGGGCACT 240
DB 181 CAGCAAAAACCTGGGCGAGGCTCCGAGGCTCCATCTATGTCATCCACAGGGCACT 240
QY 241 GGCATGCCAGACAGGTTCAAGTGCAGTGGGTCCGGGACAGACTTCACTTCCATCACT 300
DB 241 GGCATGCCAGACAGGTTCAAGTGCAGTGGGTCCGGGACAGACTTCACTTCCATCACT 300
QY 301 AACTGAGAGCTGAAAGATTTTGCAGTGTATTACTGTCAAGATATGTAAGTCACTTCA 360
DB 301 AACTGAGAGCTGAAAGATTTTGCAGTGTATTACTGTCAAGATATGTAAGTCACTTCA 360
QY 361 AACCTTCAGATACCTTTGGCGGAGGACAGAGTGAAGATCAAGCTGGCTGCA 420
DB 361 AACCTTCAGATACCTTTGGCGGAGGACAGAGTGAAGATCAAGCTGGCTGCA 420
QY 421 CCATCTGTCTCTGCGGAGTGCAGGTTCCGAGGTGTGATCAGTGAAGTGGCTCCAG 480
DB 421 TC-----CGAGCA 429
QY 481 GTTCAGCTGTGTGATCTGGGGGAGGCGTGTCCAGCTTGGGAGGTCCCTGAGATCTCC 540
DB 481 GTTCAGCTGTGTGATCTGGGGGAGGCGTGTCCAGCTTGGGAGGTCCCTGAGATCTCC 540
QY 490 GTTCAGCTGTGTGATCTGGGGGAGGCGTGTCCAGCTTGGGAGGTCCCTGAGATCTCC 549
DB 490 GTTCAGCTGTGTGATCTGGGGGAGGCGTGTCCAGCTTGGGAGGTCCCTGAGATCTCC 549
QY 541 TGTGAGGCTGTGATCTGGGGGAGGCGTGTCCAGCTTGGGAGGTCCCTGAGATCTCC 600
DB 541 TGTGAGGCTGTGATCTGGGGGAGGCGTGTCCAGCTTGGGAGGTCCCTGAGATCTCC 600
QY 601 GCGAAGGGGCTGAGTGGGTGGCACTTATCATATGATGAAGCACTAATATATCAAGCA 660
DB 601 GCGAAGGGGCTGAGTGGGTGGCACTTATCATATGATGAAGCACTAATATATCAAGCA 660
QY 661 GACTCCGTGAAGGGCGGATTCACCATCTCCAGAGCACTTCCAGAGACCGGTGATCTTA 720
DB 661 GACTCCGTGAAGGGCGGATTCACCATCTCCAGAGCACTTCCAGAGACCGGTGATCTTA 720
QY 721 AAAATGAACAGCCTGAGAACTGAGACAGGCTGTCTATTACTGTGCAAGATCAGAGC 780
DB 721 AAAATGAACAGCCTGAGAACTGAGACAGGCTGTCTATTACTGTGCAAGATCAGAGC 780
QY 730 CTGTGGGTGACTATGACCACTACTAGCGTTTGACGCTCTGGGGCAAAAGGACCAAGGCTC 789
DB 730 CTGTGGGTGACTATGACCACTACTAGCGTTTGACGCTCTGGGGCAAAAGGACCAAGGCTC 789
QY 841 ACCGTCTCCCTCAGAGATCCGAACAAAACTGATCAGCGAAGATCTGAACTCAATCCAT 900
DB 841 ACCGTCTCCCTCAGAGATCCGAACAAAACTGATCAGCGAAGATCTGAACTCAATCCAT 900
QY 901 CACCATTTAGTGAAGCTT 918
DB 901 CACCATTTAGTGAAGCTT 867

RESULT 11
AAD04540/c
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ID  AAD04540 standard; DNA; 867 BP.
XX
AC  AAD04540;
XX
DT  04-JUL-2001 (first entry)
XX
DE  Human H11-single chain variable region (scfv) complementary DNA #2.
XX
KW  Human; monoclonal antibody; Mab; H11; single chain variable region; scfv;
KW  neoplastic disease; melanoma; immunoglobulin Igm; gene therapy; lymphoma;
KW  carcinoma; breast; lung; gastric; prostate; ovary; colon; lung; vaccine;
KW  neuroblastoma; soft tissue sarcoma; prostatic adenocarcinoma; cytostatic;
KW  C-antigen; chronic leukaemia; glioma; ds.
XX
OS  Homo sapiens.
XX
PN  US6207153-B1.
XX
PD  27-MAR-2001.
XX
PF  22-MAY-1997; 97US-00862124.
XX
PR  22-MAY-1996; 96US-00657449.
XX
PA  (VIVE-) VIVENTIA BIOTECH INC.
XX
PI  Dan MD, Malti PK, Kaplan HA;
XX
DR  WPI; 2001-289584/30.
XX
PT  Composition comprising antigen binding fragments of an antibody that
PT  recognizes an antigen on neoplastic cells but not on normal cells for use
PT  in diagnosis, imaging and treatment of carcinomas.
XX
PS  Example 7; Col 71-72; 56pp; English.
XX
CC  The present sequence is human monoclonal antibody (Mab), H11-single chain
CC  variable region (scfv) complementary DNA. The invention relates to human
CC  monoclonal antibody (Mab) H11, H11-(scfv) single chain variable (V)
CC  region fragment and their corresponding DNA molecules. H11 antibody is an
CC  immunoglobulin of Igm subclass which is specific to C-antigen found
CC  specifically on neoplastic cells and not on normal cells. H11 is an
CC  antibody obtained from the fusion of peripheral blood lymphocytes of a 64
CC  year old male with a low grade glioma and fused to a human myeloma cell
CC  line to produce a hybridoma designated NBGM1/H11. A pharmaceutical
CC  composition comprising H11 and its derivatives are useful in the
CC  diagnosis, imaging and treatment of neoplastic disease, particularly,
CC  carcinoma, breast carcinoma, lung carcinoma, ovarian carcinoma, colon
CC  carcinoma, gastric carcinoma, prostate carcinoma, lymphoma carcinoma,
CC  neuroblastoma, glioma, soft tissue sarcoma, small cell lung carcinoma,
CC  prostatic adenocarcinoma, B and T cell lymphomas and chronic leukaemia.
CC  H11 DNA is also used in vaccines and gene therapy
XX
SQ  Sequence 867 BP; 189 A; 241 C; 229 G; 208 T; 0 U; 0 Other;
Query Match      86.9%; Score 798; DB 4; Length 867;
Best Local Similarity 93.9%; Pred. No. 2e-196;
Matches 862; Conservative 0; Mismatches 5; Indels 51; Gaps 1;
QY  1  GAAATTCATGAAAAAAGCGCTATCGGATCGAGTTCGCTGCTGCTTCCCTACCGTT 60
DB  867  GAAATTCATGAAAAAAGCGCTATCGGATCGAGTTCGCTGCTGCTTCCCTACCGTT 808
QY  61  GCGCAGCGCGATATTGTGTGAAGCAGTCTCCAGGACCGCTGCTTGTCTCCAGGGGAA 120
DB  807  GCGCAGCGCGATATTGTGTGAAGCAGTCTCCAGGACCGCTGCTTGTCTCCAGGGGAA 748
QY  121  AAGGCAACCTCTCTGCGAGGGCGAGTCAAGAGTTTATGAGAGCTTAAAGCTTGATAC 180
DB  747  AAGGCAACCTCTCTGCGAGGGCGAGTCAAGAGTTTATGAGAGCTTAAAGCTTGATAC 688
QY  181  CAGCAGAAACCTGGCGAGGCTCCGAGGCTCCATCATATAGTGAGTCCAGGGGCACT 240

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DB  687  CAGCAGAAACCTGGCCAGGCTCCGAGGCTTCATCATATGATGATCCAGGGCCACT 628
QY  241  GGCATGCCAGACAGGTTTCAGTGGCACTGGGTCGGGAGACACTTCACTTCACCATCACT 300
DB  627  GGCATGCCAGACAGGTTTCAGTGGCACTGGGTCGGGAGACACTTCACTTCACCATCACT 568
QY  301  AGACTGGAGCCCTGGAAGATTTTTCAGTGTATTAATCTGTCACACAGTATGATCACTTCAG 360
DB  567  AGACTGGAGCCCTGGAAGATTTTTCAGTGTATTAATCTGTCACACAGTATGATCACTTCAG 508
QY  361  ACACCTCAGATCACTTTCGCGGAGGACCAAGGTGAGATCAAGAAAGTGTGGCTGCA 420
DB  507  ACACCTCAGATCACTTTCGCGGAGGACCAAGGTGAGATCAAGAAAGTGTGGCTGCA 448
QY  421  CCATCTGTCTTGGCGGTGCGGTTCCGAGGTGTGATCAGGTGAGGTGGCTCCAG 480
DB  447  TC-----CGAGCAG 439
QY  481  GTGCAGCTGTGAGAGTCTGGGGGAGCGGTGTCAGCTGGAGGTCCCTGAGACTCTCC 540
DB  438  GTGCAGCTGTGAGAGTCTGGGGGAGCGGTGTCAGCTGGAGGTCCCTGAGACTCTCC 379
QY  541  TGTGAGCCTCTGAGATTTCCCTTCAGAAAGCTTTGCTATGACACTGGGTCCGCGAGGCTCTA 600
DB  378  TGTGAGCCTCTGAGATTTCCCTTCAGAAAGCTTTGCTATGACACTGGGTCCGCGAGGCTCTA 319
QY  601  GGCAGGGGCTGAGAGTGGGTGCGAGTTATATATATATGATGAGAGCACTAAATATCTACGCA 660
DB  318  GGCAGGGGCTGAGAGTGGGTGCGAGTTATATATATATGATGAGAGCACTAAATATCTACGCA 259
QY  661  GACTCCGTGAAGAGCGCGATTCACATCTCCAGAGACACTTCCAGAAACCGGTGTATCTTA 720
DB  258  GACTCCGTGAAGAGCGCGATTCACATCTCCAGAGACACTTCCAGAAACCGGTGTATCTTA 199
QY  721  AAAATGAACAGGCTGAGAACTGAGGACAGAGCGGTCTATTAATCTGTCGAGAGATCGAGC 780
DB  198  AAAATGAACAGGCTGAGAACTGAGGACAGAGCGGTCTATTAATCTGTCGAGAGATCGAGC 139
QY  781  CTGTTGGGTGACTATGACCACTAATCGGTTTGAAGTCTGGGGCAAAAGGACCAAGGTC 840
DB  138  CTGTTGGGTGACTATGACCACTAATCGGTTTGAAGTCTGGGGCAAAAGGACCAAGGTC 79
QY  841  ACCGCTCTCTCGAGATCCGAAACAAAACATGATCAGGAGAAAGATCTGAACCTACCAT 900
DB  78  ACCGCTCTCTCGAGATCCGAAACAAAACATGATCAGGAGAAAGATCTGAACCTACCAT 19
QY  901  CACCATTTAGTGAAGCTT 918
DB  18  CACCATTTAGTGAAGCTT 1

```

RESULT 12  
AD052300/C  
ID AD052300 standard; DNA; 867 BP.  
AC AD052300;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Human antibody H11 scfv complementary DNA #2.  
XX  
KW Antigen binding fragment; H chain V region; L chain V region; C-antigen;  
KW neoplasia; cancer; vaccine; gene therapy; human;  
KW single chain V region fragment; scfv; gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN US2004091484-A1.  
XX  
PD 13-MAY-2004.  
XX  
PF 29-AUG-2003; 2003US-00651453.



XX New T7 bacteriophage having a Fab fragment, useful for producing and  
 PT screening complex libraries of proteins that bind to particular targets,  
 PT mapping epitopes of antibodies, generating immunogens and isolating  
 PT antibodies.

XX Example 1; Fig 6a-6b; 28pp; English.

XX The present sequence is that of an anti-tetanus toxoid scFv coding  
 CC sequence. It comprises a lac promoter, an OmpA leader sequence, and  
 CC sequence encoding single chain anti-tetanus toxoid VI and VII, followed  
 CC by a His6 tag and haemagglutinin tag. The gene was used in examples from  
 CC the invention describing the construction or Fab expression constructs.  
 CC The invention relates to the T7 bacteriophage display of Fab fragments.  
 CC Host cells and methods of making the phage are described. A claimed  
 CC process for producing a Fab T7 phage display vector comprises: providing,  
 CC in the genome of a T7 phage, a first nucleic acid construct containing  
 CC nucleic acids encoding a light chain fused to a T7 capsid protein  
 CC (preferably 10a or 10b) under regulatory control of a first promoter;  
 CC and providing, in the genome of the T7 phage, a second nucleic acid construct  
 CC containing nucleic acids encoding a heavy chain Fd under the control of a  
 CC second promoter, which may be the same or different from the first  
 CC promoter.

XX Sequence 1103 BP; 243 A; 303 C; 322 G; 235 T; 0 U; 0 Other;

Query Match 49.8%; Score 457; DB 12; Length 1103;  
 Best Local Similarity 74.3%; Pred. No. 4.3e-108;  
 Matches 628; Conservative 0; Mismatches 190; Indels 27; Gaps 3;

QY 7 ATGAAAAAACCGCTATCGCGATGCGAGTTCAGCTGCGCTGCTTCCCTACCCCTGGGCGAG 66  
 DB 210 ATGAAAAAACCGCTATCGCGATGCGAGTTCAGCTGCGCTGCTTCCCTACCCCTGGGCGAG 269  
 QY 67 GCCGATATGTGTGACGAGTCTCCAGGCAACCCTCTTGTGCTCCAGGGAAAGAGCC 126  
 DB 270 GCGG---CCGAGCTCAGCAGTCTCCAGGCAACCCTCTTGTGCTCCAGGGAAAGAGCC 326  
 QY 127 ACCCTCTCTGCAAGGCGCAGTCAGAGTGTATGAGCAGTACTTAACTTGAACAGCAG 186  
 DB 327 ACCCTCTCTGCAAGGCGCAGTCAGAGTGTATGAGCAGGAGCTTAACTTGAACAGCAG 386  
 QY 187 AAACCTGGGCGAGCTCCCGAGGCTCCCTCATCTATGTGTCATCCACGAGGCGCACTGGCAG 246  
 DB 387 AAACCTGGGCGAGCTCCCGAGGCTCCCTCATCTATGTGTCATCCACGAGGCGCACTGGCAG 446  
 QY 247 CCAGACAGGTTAGTGGCAGTGGGTCGGGGAAGACCTTCACTCTCAGCATCAGTAGACTG 306  
 DB 447 CCAGACAGGTTAGTGGCAGTGGGTCGGGGAAGACCTTCACTCTCAGCATCAGTAGACTG 506  
 QY 307 GAGCCTGAAGATTTTGCAGTGTATTAAGTGTACAGCAGTATGTAGCTCACTCAGACACT 366  
 DB 507 GAGCCTGAAGATTTTGCAGTGTATTAAGTGTACAGCAGTATGTAGTGGGCTCACTCAG 560  
 QY 367 CAGATCATTCTGGGCGAGGAGCAAGGTGAGATCAAAAGCACTGTGGCTGCACCATCT 426  
 DB 561 -----TTGCGGCCCAAGGAGCAAGGTGAGATCAAAAGCACTGTGGCTGCACCATCT 611  
 QY 427 GTCTGTGGGCGTGGGCGTTCCGAGAGGTGATCGAGTGGAGGTGGCTCCAGAGTGGAG 486  
 DB 612 GGTCTGGGCGGT-----GGTGGGCGGTGTTCTCTAGATCTTCCAGAGTGGAGCTG 662  
 QY 487 CTGTGTGAGTCTGGGCGAGGCGTGTGTCAGCTGGAGAGGTCCCTGAGACTCTCTGTGCA 546  
 DB 663 CTGTGTGAGTCTGGGCGAGGCGTGTGTCAGCTGGAGAGGTCCCTGAGACTCTCTGTGCA 722  
 QY 547 GCTCTGAGATTCCTCTCAAGACTTGTGTAATGCACTGGGTCCGAGGCTCTAGGCAAG 606  
 DB 723 GCTCTGAGAGGCACTTCAAGACTTGTGTAATGCACTGGGTCCGAGGCTCTAGGCAAG 782  
 QY 607 GGGCTGAGATGGGTGCGATTTATGATGATGAGAGCACTAAATACGAGAGCTCC 666  
 DB 783 GGGCTTGAATGAGTGGAGGAGATCTTCCCTTCCGTAATACAGCAAAAGTACGACAAAC 842

QY 667 GTGAAGGGCCGATTCACCACTTCAGAGACACTTCCAGAGACGCGTATCTATAAATG 726  
 DB 843 TTCAGGGCGAGGTCCACTTACCGCGAGAAATTCACGAGCACCTTACAGAGCTG 902  
 QY 727 AACAGCCTGAGAACTGAGAGACAGCGCTGTCTATTACTGTGCGAGATGAGCCGTGG 786  
 DB 903 AGCAGCTGAGATCTGAGAGACAGCGCATATATTATTTGCGAGAGGAGATACATTTT 962  
 QY 787 GGTGACTATGACCACTACTACGTTTGAACGTCCTGGGCGAAAGGACCAAGCTACCGTC 846  
 DB 963 GGAGTGACCATGGATACTACGTTGACGTCCTGGGCGAAAGGACCAAGCTACCGTC 1022  
 QY 847 TCCTC 851  
 DB 1023 TCAC 1027

RESULT 14  
 AA250588  
 ID AA250588 standard; DNA; 1630 BP.  
 AC AA250588;  
 XX  
 DT 23-MAY-2000 (first entry)  
 XX  
 DE HD70scFv-Ck-interleukin 2 encoding DNA.  
 XX  
 KW HD70; single-chain variable fragment; scFv; 17-1A antigen; human; BpCAM;  
 KW epithelial cell adhesion molecule; inflammatory cytokine; IL-2;  
 KW interleukin-2; Ck-domain; kappa light chain constant domain;  
 KW heteroantibody; multifunctional compound; immunoglobulin; cyostatic;  
 KW immunostimulatory; antileukemia; diagnosis; prevention;  
 KW antiproliferative; treatment; malignant; haematopoietic cell; lymphoma;  
 KW leukaemia; solid tumour; carcinoma; melanoma; sarcoma; ds.  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FT CDS 39..1613  
 FT /\*tag= a  
 FT /product= "HD70scFv-Ck-IL-2 chain"  
 FT /\*tag= b  
 FT /label= HD70\_scFv  
 XX  
 PN MO200006605-A2.  
 XX  
 PD 10-FEB-2000.  
 XX  
 XX 28-JUL-1999; 99WO-BP005416.  
 PF  
 XX  
 PR 28-JUL-1998; 98EP-00114082.  
 XX  
 PA (MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.  
 XX  
 PI Kufer P, Dreier T, Baeuerle PA, Borschert K, Zettl F;  
 XX  
 DR WPI; 2000-195265/17.  
 DR P-PSDB; AA4495.  
 XX  
 PT New multifunctional compounds useful for preventing and/or treating  
 PT malignant cell growth and for detection and diagnosis.  
 XX  
 PS Claim 8; Fig 55B; 166pp; English.  
 XX  
 CC The patent discloses heteroantibodies which are multifunctional compounds  
 CC producible in a mammalian host cell as a secretable and fully functional  
 CC heterodimer of two polypeptide chains, where one of the polypeptide  
 CC chains comprises a CH1-domain (constant domain of an immunoglobulin  
 CC heavy chain) and the other chain comprises CL-domain (constant domain of  
 CC an immunoglobulin light chain). The polypeptide chains further comprise,  
 CC fused to the constant domains at least two (poly)peptides having

CC different receptor or ligand functions, where further at least two of the  
 CC different (poly)peptides lack an intrinsic affinity for one another and  
 CC are linked via the constant domains. The heteromibodies have  
 CC cytostatic, immunostimulatory, antileukemia and antiproliferative  
 CC activities. These compounds can be used for diagnosing, preventing and  
 CC treating malignant cell growth related to malignancies of haematopoietic  
 CC cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,  
 CC melanomas and sarcomas. The present sequence is a DNA encoding right  
 CC chain of a heteromibody comprising HD70 single-chain Fv (scFv) fragment  
 CC N-terminally linked to human Ck domain (constant domain of immunoglobulin  
 CC -kappa light chain) which bears at its C-terminus the human inflammatory  
 CC cytokine interleukin-2 (IL-2). HD70 scFv specifically recognises the  
 CC human epithelial cell adhesion molecule (EPCAM) also called 17-1A antigen

XX Sequence 1630 BP; 445 A; 410 C; 408 G; 367 T; 0 U; 0 Other;

SQ Query Match 48.5%; Score 445; DB 3; Length 1630;

Best Local Similarity 76.3%; Pred. No. 6,1e-105; Mismatches 145; Indels 48; Gaps 4;

Matches 620; Conservative 0; Mismatches 145; Indels 48; Gaps 4;

52 GCTACCGTTCGCGAGCCGATATGTTGTGACGAGCTTCCAGGCACTCTGTTGCT 111  
 78 GCTACAGGTGTACCTCCAGAGCTCCAGATGACCCAGTCTCCATCTCCCTGCTGCATCT 137

112 CCAGGGGAAAGCCACCTCTCTCCAGAGGCCAGTCAGAGTGTAGTAGAGCTACTTA 171  
 138 GTAGGAGACAGAGATCCATCACTTCCGCGCAAGTCAGAG---CATTAGCAGCTATTTA 194

172 GCCTGTACAGAGAAACCTGCGCAGGCTCCAGGCTCCCTCATCTATGATGATCACC 231  
 195 AATGGTATCAGAGAAACAGAGACAGCTCCCTCAAGCTGCTCATTTACTGGGATCTACC 254

232 AGGGCCACTGGCAGATGCGCAAGGTTCAAGTGCAGTGGGTCCGGGACAGACTTACTCTC 291  
 255 CCGGAATCCGGGGTCCCTGATCCGATTCAGGCGAGTGAATCTGGGACAAATTACACTCTC 314

292 ACCATAGTAGAGTGAAGCTGAGCTGAGTTTGGAGTGTATTAAGTGTAGAGATAGTAC 351  
 315 ACCATAGAGAGCTGAGAGCTGAGAAATTTGCTAATTAATTTGTAACAGTGTGACAGT 374

352 TCACCTCAGACACCTCAGATCACTTTCGGGCGAGGAGCCAAAGTGAAGATCAACAACAT 411  
 375 TTGCC-----GATCACTTCGCGCAAGGAGACAGATGACATTCAA----- 416

412 GTGGCTGACCATCTGTCTCTGCGGGTGGCGGTTCCGAGGTGTGATCAGGTGAGGT 471  
 417 -----GGAGGAGGAGATCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 455

472 GGCTCCAGGTGAGCTGTGTGAGTGTGGGAGGGGTGTGTGACGCTGGGAGGTCCG 531  
 456 GGCTCAGAGGTGAGCTGTGTGAGTGTGGGAGGGGTGTGTGACGCTGGGAGGTCCG 515

532 AGACTCTCTGTGACGCTGTGATTCCTCTCAGAAAGCTTTGCTATGCACTGGTCCG 591  
 516 AGACTCTCTGTGACGCTGTGATTCCTCTCAGAAAGCTTTGCTATGCACTGGTCCG 575

592 CAGGCTCTAGGCAAGGGGCTGAGGTGGTGGCAGTTATCATATATATATATATATATAT 651  
 576 CAGGCTCTAGGCAAGGGGCTGAGGTGGTGGCAGTTATCATATATATATATATATATAT 635

652 TATATAGGAGATCTCGTGAAGGGGCGATTCACATCTCCAGAGACAAATTCAGAAACAG 711  
 636 TATATAGGAGATCTCGTGAAGGGGCGATTCACATCTCCAGAGACAAATTCAGAAACAG 695

712 GTGTATCTATAAATGAACAGCTGAGATGAGAGACAGGCTGTCTATTTACTGTGAGAG 771  
 696 CTGTATCTGTGAATGAACAGCTGAGATGAGAGACAGGCTGTCTATTTACTGTGAGAA 755

772 GATCAGAGCTGTGTGGTACT-----ATGACCACTACTAGCGTTTGAAGCTGTGGGCG 825  
 756 GATATGGGGTGGGAGTGGCTGGAAGACCTACTACTACTAGCGTATGAGCGTCTGGGCG 815

826 AAAGGAGCACCGGTCAACCGTCTCTCTCAGAGATCC 858

DB 816 CAAAGGACCAACGGTACCCGTCTCTCCGGAAC 848

RESULT 15  
 AA250587  
 AA250587 strand; DNA; 1630 BP.

AA250587,

23-MAY-2000 (first entry)

DE HD70scFv-CH1-GM-CSF chain encoding DNA.

XX HD70, single-chain variable fragment; scFv; 17-1A antigen; human; EPCAM;  
 KW epithelial cell adhesion molecule; inflammatory cytokine; GM-CSF;  
 KW granulocyte/macrophage colony stimulating factor; heteromibody;  
 KW CH1-domain; multifunctional compound; heavy chain constant domain;  
 KW immunoglobulin; cytostatic; immunostimulatory; antileukemia; diagnosis;  
 KW antiproliferative; prevention; treatment; malignant; haematopoietic cell;  
 KW lymphoma; leukaemia; solid tumour; carcinoma; melanoma; sarcoma; ds.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FH CDS 39..1610  
 FT /\*tag= a  
 FT /product= "HD70scFv-CH1-GM-CSF chain"  
 FT /\*tag= b  
 FT /\*label= HD70\_scFv

XX MO200006605-A2.

XX 10-FEB-2000.

XX 28-JUL-1999; 99WC-EP005416.

XX 28-JUL-1998; 98EP-00114082.

XX (MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.

XX Kufer F, Dreier T, Baeuerle PA, Borschert K, Zetcl F;

XX WPI; 2000-195265/17.

XX P-PSDB; AAY44994.

XX New multifunctional compounds useful for preventing and/or treating

XX malignant cell growth and for detection and diagnosis.

XX Claim 8, Fig 55A, 166pp, English.

CC The patent discloses heteromibodies which are multifunctional compounds  
 CC producible in a mammalian host cell as a secretable and fully functional  
 CC heterodimer of two polypeptide chains, where one of the polypeptide  
 CC chains comprises a CH1-domain (constant domain of an immunoglobulin  
 CC heavy chain) and the other chain comprises C1-domain (constant domain of  
 CC an immunoglobulin light chain). The polypeptide chains further comprise,  
 CC fused to the constant domains at least two (poly)peptides having  
 CC different receptor or ligand functions, where further at least two of the  
 CC different (poly)peptides lack an intrinsic affinity for one another and  
 CC are linked via the constant domains. The heteromibodies have  
 CC cytostatic, immunostimulatory, antileukemia and antiproliferative  
 CC activities. These compounds can be used for diagnosing, preventing and  
 CC treating malignant cell growth related to malignancies of haematopoietic  
 CC cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,  
 CC melanomas and sarcomas. The present sequence is a DNA encoding left chain  
 CC of a heteromibody comprising HD70 single-chain Fv (scFv) fragment N-  
 CC terminally linked to human CH1 domain which bears at its C-terminus the  
 CC human inflammatory cytokine granulocyte/macrophage colony stimulating  
 CC factor (GM-CSF), plus a hexahistidine sequence for ease of purification.  
 CC HD70 scFv specifically recognises the human epithelial cell adhesion  
 CC molecule (EPCAM) also called 17-1A antigen

XX Sequence 1630 BP; 376 A; 484 C; 437 G; 333 T; 0 U; 0 Other;

Query Match 48.5%; Score 445; DB 3; Length 1630;  
Best Local Similarity 76.3%; Pred. No: 6.1e-105;  
Matches 620; Conservative 0; Mismatches 145; Indels 48; Gaps 4;

QY 52 GCTACCGTTGCGAGGCCCATATTTGTTGACGACAGTCTTCAGGCACTCTTGTCT 111  
DB 78 GCTACAGGTGTATACCTCCAGCTCCAGATGACCAGTCTCCATCTCCCTGTCTGACAT 137  
QY 112 CCAGGGGAAAGAGCCACCTCTCTCTGACGGCCAGTCAAGTGTATAGCAGCTACTTA 171  
DB 138 GTAGGAGACAGACTCCATCACTTCCGGGCAAGTCAGG---CATTAGCACTATTTA 194  
QY 172 GCTGTGTACAGAGAACTGTGGCAGGCTCCAGGCTCTCATCTATGTGTGATCCACC 231  
DB 195 AATTGGTATCAGCAGAAACAGGACAGCTCTTAAGCTGCTCATTTACTGGGCATCACC 254  
QY 232 AGGGCCACTGGCATGTCAGACAGTTCAGTGGCAGTGGGTCCGGACAGACTTCACTTC 291  
DB 255 CCGGAATCCGGGTCTCTGACCATCCGATCAGCGGCAATGGAATCTGGGACAAATTACACTTC 314  
QY 292 ACCATCAGTAGACTGAGGCTGAAATTTTGACGTATTACTGTACAGCAGTATGATAGC 351  
DB 315 ACCATCAGCAGCTTGACAGCTTGAAATTTTGCTACTTCTTGTCAACAGCTGACAGT 374  
QY 352 TCACCTCAGACACCTCAGATCACTTTCGGCGAGGAGCCAAAGGTGAGATCAACGACT 411  
DB 375 TTGCC-----GATCACCTTCGGGCAAGGACAGACTGACATTCNA----- 416  
QY 412 GTGGCTGCACCATCTGTCTGTGGCGGTGGCGGTTCCGAGGTGTGATCAGGTGAGGT 471  
DB 417 -----GGAGGAGAGGATCAGGTGTGTGTAGCGCGCGCGC 455  
QY 472 GGTCCAGAGTGCAGCTGTGAGTCTGGGGGAGGCGGTGCCAGCTGGGAGGTCCCTG 531  
DB 456 GGTCTAGAGGTGCAGCTGTGAGTCTGGGGGAGGCGGTGCCAGCTGGGAGGTCCCTG 515  
QY 532 AGACTCTCTGTGACAGCTCTGGAATCCCTTCAGAAAGCTTGTCTATGCACTGGGTCCG 591  
DB 516 AGACTCTCTGTGACAGCTCTGGAATCATTCAAGTATGATGCACTGGGTCCG 575  
QY 592 CAGGCTCTAGGCAAGGGGCTGAGGTGGTGGCAGTTATCATATGATGAAAGCACTAAA 651  
DB 576 CAGGCTCCAGGCAAGGGGCTGAGGTGGTGGCAGTTATCATATGATGAAAGTAAATAA 635  
QY 652 TACTACGAGACTCCGTTGAAGGCGGATTCAACATCTCCAGAGACACTTCCAAGAACAG 711  
DB 636 TACTATGACAGCTCCGTTGAAGGCGGATTCAACATCTCCAGAGACAAATCCAAGAACAG 695  
QY 712 GTGTATCTTAAATGAACAGCTGAGAACTGAGAACACGGCTGTCTATTACTGTGCGAGA 771  
DB 696 CTGTATCTGCAATGAACAGCTGAGAGCTGAGAGACACGGCTGTCTATTACTGTGCGAAA 755  
QY 772 GATCAGAGCTGTGGGTGACT-----ATGACCACTACTACGTTTGAACGTCTGGGCG 825  
DB 756 GATATGGGCTGGGCGAGTGGCTGAGAACCTTACTACTACGATATGAGCGTCTGGGCG 815  
QY 826 AAAGGAGCAGGCTCACCGTCTCCCTCAGGATCC 858  
DB 816 CAAGGAGCAGGCTCACCGTCTCCCTCAGGATCC 848

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Job time : 624 secs

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OM nucleic - nucleic search, using bw model

Run on: February 18, 2005, 05:23:45 ; Search time 203 Seconds

(Without alignments)  
7399.517 Million cell updates/sec

Title: US-09-194-164-13

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	918	100.0	918	3	US-08-862-124-13 Sequence 13, Appl
2	916.4	99.8	918	3	US-08-862-124-15 Sequence 15, Appl
3	799.6	87.1	867	3	US-08-862-124-16 Sequence 16, Appl
4	798	86.9	867	3	US-08-862-124-18 Sequence 18, Appl
5	361	39.3	450	3	US-08-862-124-6 Sequence 6, Appl
6	359.4	39.2	450	3	US-08-862-124-4 Sequence 4, Appl
7	345.2	37.6	783	1	US-08-487-283A-19 Sequence 19, Appl
8	343.6	37.4	1848	1	US-08-447-422-15 Sequence 15, Appl
9	324.4	35.3	543	3	US-08-862-124-1 Sequence 1, Appl
10	324.4	35.3	543	3	US-08-862-124-3 Sequence 3, Appl
11	319.8	34.8	1413	4	US-09-472-087-61 Sequence 61, Appl
12	318.4	34.7	4691	3	US-09-591-632-43 Sequence 43, Appl
13	318.4	34.7	4691	3	US-09-611-451-43 Sequence 43, Appl
14	318.4	34.7	6166	3	US-08-591-632-51 Sequence 51, Appl
15	318.4	34.7	6166	3	US-09-611-451-51 Sequence 51, Appl
16	310.6	33.8	678	4	US-09-456-090A-49 Sequence 49, Appl
17	310.6	33.8	678	4	US-09-456-090A-85 Sequence 85, Appl
18	310.6	33.8	678	4	US-09-453-234-49 Sequence 49, Appl
19	310.6	33.8	678	4	US-09-453-234-85 Sequence 85, Appl
20	305.8	33.3	678	4	US-09-456-090A-37 Sequence 37, Appl
21	305.8	33.3	678	4	US-09-456-090A-41 Sequence 41, Appl
22	305.8	33.3	678	4	US-09-456-090A-71 Sequence 71, Appl
23	305.8	33.3	678	4	US-09-453-234-37 Sequence 37, Appl
24	305.8	33.3	678	4	US-09-453-234-41 Sequence 41, Appl
25	305.8	33.3	678	4	US-09-453-234-71 Sequence 71, Appl
26	303.6	33.1	1797	1	US-08-442-542-17 Sequence 17, Appl
27	303.6	33.1	1797	3	US-08-765-469-17 Sequence 17, Appl

28	303.4	33.1	369	4	US-09-424-840B-5 Sequence 5, Appl
29	302.6	33.0	678	4	US-09-456-090A-73 Sequence 73, Appl
30	302.6	33.0	678	4	US-09-453-234-73 Sequence 73, Appl
31	301	32.8	678	4	US-09-456-090A-79 Sequence 79, Appl
32	301	32.8	678	4	US-09-453-234-79 Sequence 79, Appl
33	301	32.8	948	4	US-09-859-053-33 Sequence 33, Appl
34	300.6	32.7	752	6	5455030-12 Patent No. 5455030
35	300.6	32.7	752	6	5455030-12 Patent No. 5455030
36	300.2	32.7	672	4	US-09-456-090A-51 Sequence 51, Appl
37	300.2	32.7	672	4	US-09-453-234-51 Sequence 51, Appl
38	299.8	32.7	708	4	US-09-472-087-40 Sequence 40, Appl
39	299.8	32.7	708	4	US-09-472-087-56 Sequence 56, Appl
40	299.4	32.6	970	4	US-09-859-053-37 Sequence 37, Appl
41	298.2	32.5	372	4	US-09-424-840B-15 Sequence 15, Appl
42	297	32.4	672	4	US-09-456-090A-39 Sequence 39, Appl
43	297	32.4	672	4	US-09-456-090A-75 Sequence 75, Appl
44	297	32.4	672	4	US-09-453-234-39 Sequence 39, Appl
45	297	32.4	672	4	US-09-453-234-75 Sequence 75, Appl

#### ALIGNMENTS

RESULT 1  
US-08-862-124-13  
Sequence 13, Application US/08862124  
Patent No. 6207153  
GENERAL INFORMATION:  
APPLICANT: Dan, Michael D.  
APPLICANT: Malti, Pradip K.  
TITLE OF INVENTION: KAPLAN, Howard A.  
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND TREATMENT OF CANCERS  
TITLE OF INVENTION: DETECTION OF CANCERS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster LLP  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/862,124  
FILING DATE: 22-MAY-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Lehnardt, Susan K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 31608-20001.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 918 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: join(1..906, 913..918)  
US-08-862-124-13  
Query Match 100.0%; Score 918; DB 3; Length 918;  
Best Local Similarity 100.0%; Pred. No. 1.8e-252;

Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCATGAAAAAACCCTATTCGCGATGCGAGTTGCACTGGCTGGTTCCTACCGTT 60

Db 1 GAATTCATGAAAAAACCCTATTCGCGATGCGAGTTGCACTGGCTGGTTCCTACCGTT 60

QY 61 GGCAGAGCCGATATTGTGTGAAGCAAGTCTCAAGGACCTGTCTTTGTCTCCAGGGGAA 120

Db 61 GGCAGAGCCGATATTGTGTGAAGCAAGTCTCAAGGACCTGTCTTTGTCTCCAGGGGAA 120

QY 121 AAGAGCCACCTCTCCGCGAGGCGACAGAGTTAGTAGAGCACTTAGGCTGGTAC 180

Db 121 AAGAGCCACCTCTCCGCGAGGCGACAGAGTTAGTAGAGCACTTAGGCTGGTAC 180

QY 181 CAGCAGAAAACCTGGCCAGGCTCCAGAGCTCTCATCTATGATGATCAACAGGCGCACT 240

Db 181 CAGCAGAAAACCTGGCCAGGCTCCAGAGCTCTCATCTATGATGATCAACAGGCGCACT 240

QY 241 GGCATGCCAGACAGTTCAAGTGGAGTGGGTCGGGACAGACTTCACTCTCACCATCAGT 300

Db 241 GGCATGCCAGACAGTTCAAGTGGAGTGGGTCGGGACAGACTTCACTCTCACCATCAGT 300

QY 301 AAGCTGGAGCCCTGAAGATTTTGAAGTATTACTGTCAAGAGTATGATGATGATGATGAT 360

Db 301 AAGCTGGAGCCCTGAAGATTTTGAAGTATTACTGTCAAGAGTATGATGATGATGATGAT 360

QY 361 ACACCTCAGATCACTTTCGCGAGGAGACCAAGGTGAGATCAAAAGAACTGTGGCTGCA 420

Db 361 ACACCTCAGATCACTTTCGCGAGGAGACCAAGGTGAGATCAAAAGAACTGTGGCTGCA 420

QY 421 CCATCTGTCTCTGGCGGCGGCTTCGGAAGTGTGATCAGGTGAGAGTGGCTCCAG 480

Db 421 CCATCTGTCTCTGGCGGCGGCTTCGGAAGTGTGATCAGGTGAGAGTGGCTCCAG 480

QY 481 GTGCAGCTGTGAGTCTGGGGAGGCGGTGATCAGCTGGGAGGTCCCTGAGACTCTCC 540

Db 481 GTGCAGCTGTGAGTCTGGGGAGGCGGTGATCAGCTGGGAGGTCCCTGAGACTCTCC 540

QY 541 TGTGACAGCTGTGATTTCCCTTCAGAAAGCTTTGCTATGCACTGGGTCCGCGAGCTCT 600

Db 541 TGTGACAGCTGTGATTTCCCTTCAGAAAGCTTTGCTATGCACTGGGTCCGCGAGCTCT 600

QY 601 GGCAGAGGCGTGAAGTGGTGGCGAGTTATCATATGATGAGCACTAAATCTAGCGCA 660

Db 601 GGCAGAGGCGTGAAGTGGTGGCGAGTTATCATATGATGAGCACTAAATCTAGCGCA 660

QY 661 GACTCGGTGAAGGCGGATTCACCATCTCCAGAGCACTTCCAAAGAACAGGATCTCTA 720

Db 661 GACTCGGTGAAGGCGGATTCACCATCTCCAGAGCACTTCCAAAGAACAGGATCTCTA 720

QY 721 AAAATGAACGCTTGAGAACTGAGACACGCTGTCTATTACTGTGCGAGAGATCAGAGC 780

Db 721 AAAATGAACGCTTGAGAACTGAGACACGCTGTCTATTACTGTGCGAGAGATCAGAGC 780

QY 781 CTGTGGGTGATCTATGACCTACTACGTTTGGAGCTCTGGGGCAAAAGGACCAAGCTC 840

Db 781 CTGTGGGTGATCTATGACCTACTACGTTTGGAGCTCTGGGGCAAAAGGACCAAGCTC 840

QY 841 ACCGTCTCCAGAGATCCGAAACAAAATGATCAGGGAAGAATCTGAACCATCAGCAT 900

Db 841 ACCGTCTCCAGAGATCCGAAACAAAATGATCAGGGAAGAATCTGAACCATCAGCAT 900

QY 901 CACCATTAATGAAGCTT 918

Db 901 CACCATTAATGAAGCTT 918

RESULT 2  
US-08-862-124-15/c  
; Sequence 15, Application US/08862124  
; Patent No. 6207153  
; GENERAL INFORMATION:  
; APPLICANT: Dan, Michael D.

APPLICANT: Maiz, Pradi K.  
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H1, THAT  
SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE  
TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE  
TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE  
TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster LLP  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 22-MAY-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Lehnardt, Susan K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 31608-20001.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 918 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-862-124-15

Query Match 99.8%; Score 916.4; DB 3; Length 918;  
Best Local Similarity 99.9%; Pred. No. 5.1e-252;  
Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAATTCATGAAAAAACCCTATTCGCGATGCGAGTTGCACTGGCTGGTTCCTACCGTT 60

Db 918 GAATTCATGAAAAAACCCTATTCGCGATGCGAGTTGCACTGGCTGGTTCCTACCGTT 859

QY 61 GGCAGAGCCGATATTGTGTGAAGCAAGTCTCAAGGACCTGTCTTTGTCTCCAGGGGAA 120

Db 61 GGCAGAGCCGATATTGTGTGAAGCAAGTCTCAAGGACCTGTCTTTGTCTCCAGGGGAA 799

QY 121 AAGAGCCACCTCTCTCGAGGCGACAGAGTTAGTAGAGCACTTAGGCTGGTAC 180

Db 121 AAGAGCCACCTCTCTCGAGGCGACAGAGTTAGTAGAGCACTTAGGCTGGTAC 739

QY 181 CAGCAGAAAACCTGGCCAGGCTCCAGAGCTCTCATCTATGATGATCAACAGGCGCACT 240

Db 181 CAGCAGAAAACCTGGCCAGGCTCCAGAGCTCTCATCTATGATGATCAACAGGCGCACT 679

QY 241 GGCATGCCAGACAGTTCAAGTGGAGTGGGTCGGGACAGACTTCACTCTCACCATCAGT 300

Db 241 GGCATGCCAGACAGTTCAAGTGGAGTGGGTCGGGACAGACTTCACTCTCACCATCAGT 619

QY 301 AAGCTGGAGCCCTGAAGATTTTGAAGTATTACTGTCAAGAGTATGATGATGATGATGAT 360

Db 301 AAGCTGGAGCCCTGAAGATTTTGAAGTATTACTGTCAAGAGTATGATGATGATGATGAT 559

QY 361 ACACCTCAGATCACTTTCGCGAGGAGACCAAGGTGAGATCAAAAGAACTGTGGCTGCA 420

Db 361 ACACCTCAGATCACTTTCGCGAGGAGACCAAGGTGAGATCAAAAGAACTGTGGCTGCA 499

QY 421 CCATCTGTCTCTGGCGGCGGCTTCGGAAGTGTGATCAGGTGAGAGTGGCTCCAG 480



498 CCATCTGCTCTGGCGGTGGCGGTTCCGAGGCTGATCAAGTGGAGTGGCTCCAG 439  
QY 481 GTGCAGCTGGTGAAGTCTGGGGGAGGCGGTGTCACGCTGGAGAGTCCCTGAGACTCTCC 540  
Db 438 GTGCAGCTGGTGAAGTCTGGGGGAGGCGGTGTCACGCTGGAGAGTCCCTGAGACTCTCC 379  
QY 541 TGTGAGGCTCTGAGATTCCTTCAGAACTTGTAGTGCATGGGTCCGCGAGGCTCA 600  
Db 378 TGTGAGGCTCTGAGATTCCTTCAGAACTTGTAGTGCATGGGTCCGCGAGGCTCA 319  
QY 601 GGCAGAGGCTGAGAGTGGGTGCGAGTTATCATATGATGAGAGCACTAAATACACGA 660  
Db 318 GGCAGAGGCTGAGAGTGGGTGCGAGTTATCATATGATGAGAGCACTAAATACACGA 259  
QY 661 GACTCCGTGAAGGCGCGATTCACCATCTTCAGAGACACTTCCAGAAACGCGTGTACTA 720  
Db 258 GACTCCGTGAAGGCGCGATTCACCATCTTCAGAGACACTTCCAGAAACGCGTGTACTA 199  
QY 721 AAAATGAACAGCTGAGACCTGAGGACAGCGCTGTCTATTAAGTGGAGAGATGAGAGC 780  
Db 198 AAAATGAACAGCTGAGACCTGAGGACAGCGCTGTCTATTAAGTGGAGAGATGAGAGC 139  
QY 781 CTGTTGGGTGACTATGACCACTACTACGGTTTGAAGTCTGGGGGCAAAAGGACACGCTC 840  
Db 138 CTGTTGGGTGACTATGACCACTACTACGGTTTGAAGTCTGGGGGCAAAAGGACACGCTC 79  
QY 841 ACCGTCTCTCAGATTCGGAACAAAACTGATCAGCGAAGAGATCTGAACCATGACCAT 900  
Db 78 ACCGTCTCTCAGATTCGGAACAAAACTGATCAGCGAAGAGATCTGAACCATGACCAT 19  
QY 901 CACCATTAAGTGAAGCTT 918  
Db 18 CACCATTAAGTGAAGCTT 1

## RESULT 3

US-08-862-124-16

Sequence 16, Application US/08862124

Patent No. 6207153

GENERAL INFORMATION:

APPLICANT: Dan, Michael D.

APPLICANT: Maiti, Pradipt K.

APPLICANT: Kaplan, Howard A.

TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H1, THAT

TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE

TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison &amp; Foerster LLP

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/862,124

FILING DATE: 22-MAY-1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Lehnardt, Susan K.

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 31608-20001.20

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 813-5600

TELEFAX: (650) 494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:  
LENGTH: 867 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: join(1..855, 862..867)  
US-08-862-124-16

Query Match 87.1%; Score 799.6; DB 3; Length 867;  
Best Local Similarity 94.0%; Pred. No. 1.3e-218;  
Matches 863; Conservative 0; Mismatches 4; Indels 51; Gaps 1;

1 GAATTCATGAAAAAACCCTATATCGCATGCGAGTTGCACTGGCTGGTTGCTACCGTT 60  
Db 1 GAATTCATGAAAAAACCCTATATCGCATGCGAGTTGCACTGGCTGGTTGCTACCGTT 60  
QY 61 GGCAGGCGCGAATATGTTGTTGACGCAAGTCTCAGAGCAACCTGTTCTTCTCAAGGAA 120  
Db 61 GGCAGGCGCGAATATGTTGTTGACGCAAGTCTCAGAGCAACCTGTTCTTCTCAAGGAA 120  
QY 121 AGAGCCACCCTCTCCTGCAAGGCGCAGTCAAGATGTTAGTGAAGCACTTACCTGGTAC 180  
Db 121 AGAGCCACCCTCTCCTGCAAGGCGCAGTCAAGATGTTAGTGAAGCACTTACCTGGTAC 180  
QY 181 CAGCAAAAACCTGCGCAGGCTTCCAGGCTCCTCATCTATGTTGATCCACAGGGCACT 240  
Db 181 CAGCAAAAACCTGCGCAGGCTTCCAGGCTCCTCATCTATGTTGATCCACAGGGCACT 240  
QY 241 GGCATGCCAGACAGGTTCAATGTCAGTGGGTCCGGGACAGACTTCACTTCAACATCACT 300  
Db 241 GGCATGCCAGACAGGTTCAATGTCAGTGGGTCCGGGACAGACTTCACTTCAACATCACT 300  
QY 301 AGACTGAGCCCTGAAGATTTTTCAGTGTATTAATGTCAGCAGATGATGATGATGATGAT 360  
Db 301 AGACTGAGCCCTGAAGATTTTTCAGTGTATTAATGTCAGCAGATGATGATGATGATGAT 360  
QY 361 ACACCTCAGATCACTTTCCGCGAGGAGCAAGGTGAGATCAAAAGAACTGTGCTGCA 420  
Db 361 ACACCTCAGATCACTTTCCGCGAGGAGCAAGGTGAGATCAAAAGAACTGTGCTGCA 420  
QY 421 CCATCTGCTCTGGGCGGTGGCGGTTCCGAGGTGATCAGTGGAGGTGGTCCGAG 480  
Db 421 TC-----CGAGCAG 429  
QY 481 GTGCAGCTGGTGAAGTCTGGGGGAGCGGTGTCACGCTGGAGGCTCTGAGACTCTCC 540  
Db 430 GTGCAGCTGGTGAAGTCTGGGGGAGCGGTGTCACGCTGGAGGCTCTGAGACTCTCC 489  
QY 541 TGTGAGGCTCTGAGATTCCTTCAGAACTTGTGATGCACTGGGTCCGCGAGGCTCTA 600  
Db 490 TGTGAGGCTCTGAGATTCCTTCAGAACTTGTGATGCACTGGGTCCGCGAGGCTCTA 549  
QY 601 GGCAGAGGCTGAGAGTGGGTGCGCACTTATCATATGATGAGAGCACTAAATACACGA 660  
Db 550 GGCAGAGGCTGAGAGTGGGTGCGCACTTATCATATGATGAGAGCACTAAATACACGA 609  
QY 661 GACTCCGTGAAGGCGCGATTACCATCTCCAGAGCACTTCCAGAAACGCGTGTACTCA 720  
Db 610 GACTCCGTGAAGGCGCGATTACCATCTCCAGAGCACTTCCAGAAACGCGTGTACTCA 669  
QY 721 AAAATGAACAGCTGAGAACTGAGGACACGCGTGTCTATTACTGTGCGAGATGAGAGC 780  
Db 670 AAAATGAACAGCTGAGAACTGAGGACACGCGTGTCTATTACTGTGCGAGATGAGAGC 729  
QY 781 CTGTTGGGTGACTATGACCACTACTACGGTTTGAAGTCTGGGGGCAAAAGGACACGCTC 840  
Db 730 CTGTTGGGTGACTATGACCACTACTACGGTTTGAAGTCTGGGGGCAAAAGGACACGCTC 789  
QY 841 ACCGTCTCTCAGAGATTCGGAACAAAACTGATCAGCGAAGAGATCTGAACCATGACCAT 900  
Db 790 ACCGTCTCTCAGAGATTCGGAACAAAACTGATCAGCGAAGAGATCTGAACCATGACCAT 849



```

1 APPLICATION NUMBER: US/08/862,124
2 FILING DATE: 22-MAY-1997
3 CLASSIFICATION: 424
4 ATTORNEY/AGENT INFORMATION:
5 NAME: Lehnhardt, Susan K.
6 REGISTRATION NUMBER: 33,943
7 REFERENCE/DOCKET NUMBER: 31608-20001.20
8 TELECOMMUNICATION INFORMATION:
9 TELEPHONE: (650) 813-5600
10 TELEFAX: (650) 494-0792
11 TELEX: 706141
12 INFORMATION FOR SEQ ID NO: 6:
13 SEQUENCE CHARACTERISTICS:
14 LENGTH: 450 base pairs
15 TYPE: nucleic acid
16 STRANDEDNESS: double
17 TOPOLOGY: linear
18 JS-08-862-124-6

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Query Match	39.3%	Score 361	DB 3	Length 450
Best Local Similarity	100.0%	Pred. NO.	2.7e-93	
Matches 361		Conservative	0	Indels 0
		Mismatches	0	Gaps 0

Qy	70	GATATTGTTGACGAGCTCCAGGCA	CCCTGTCTTTGTCTCCAGGGGAAAGGCACC	12
Db	378	GATATTGTGTGACGAGCTCCAGGCA	CCCTGTCTTTGTCTCCAGGGGAAAGGCACC	318
Qy	130	CTCTCTGCAGGGCCAGTCAGAGTGT	TGTTAGTACAGCTATTAGCTGTGATCCAGAGAA	188
Db	318	CTCTCTGCAGGGCCAGTCAGAGTGT	TGTTAGTACAGCTATTAGCTGTGATCCAGAGAA	255
Qy	190	CTTGCCGAGGCTCCAGGCTCCTCAT	CTTAGTGATCCACGAGGCACCTGGCATGCCA	248
Db	258	CTTGCCGAGGCTCCAGGCTCCTCAT	CTTAGTGATCCACGAGGCACCTGGCATGCCA	198
Qy	250	GACAGGTCAGTGGCGAGTGGGTCCG	GGACAGCTTCACTCTCACATACATGATGACTGAG	308
Db	198	GACAGGTCAGTGGCGAGTGGGTCCG	GGACAGCTTCACTCTCACATACATGATGACTGAG	138
Qy	310	CCGGAAGATTTTGCAGTGTATTACTG	CAGCAGTATGTTACTCACTCAGACACTCAG	368
Db	138	CCGGAAGATTTTGCAGTGTATTACTG	CAGCAGTATGTTACTCACTCAGACACTCAG	78
Qy	370	ATCATTTCGGCGGAGGACCAAGGTG	AGATCAACGAACTGTGGCTGCACATCTGT	428
Db	78	ATCATTTCGGCGGAGGACCAAGGTG	AGATCAACGAACTGTGGCTGCACATCTGT	18
Qy	430	T	430	
Db	18	T	18	

RESULT 6  
US-08-862-124-4  
; Sequence 4, Application US/08862124  
; Patent No. 6207153

```

1  APPLICANT:  Dan, Michael D.
2  APPLICANT:  Matci, Pradiip K.
3  APPLICANT:  Kaplan, Howard A.
4  TITLE OF INVENTION:  ANTIGEN BINDING FRAGMENTS H11, THAT
5  TITLE OF INVENTION:  SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
6  TITLE OF INVENTION:  FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
7  TITLE OF INVENTION:  DETECTION OF CANCERS
8  NUMBER OF SEQUENCES:  28
9  CORRESPONDENCE ADDRESS:
10 ADDRESS:  Morrison & Foerster LLP
11 STREET:  755 Page Mill Road
12 CITY:  Palo Alto
13 STATE:  CA
14 COUNTRY:  USA
15 ZIP:  94304-1018
16 COMPUTER READABLE FORM:

```

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1      MEDIUM TYPE: Floppy disk
2      COMPUTER: IBM PC compatible
3      OPERATING SYSTEM: PC-DOS/MS-DOS
4      SOFTWARE: PatentIn Release #1.0, Versid
5      CURRENT APPLICATION DATA:
6      APPLICATION NUMBER: US/08/862,124
7      FILING DATE: 22-MAY-1997
8      CLASSIFICATION: 424
9      ATTORNEY/AGENT INFORMATION:
10     NAME: Lehnhardt, Susan K.
11     REGISTRATION NUMBER: 33,943
12     REFERENCE/DOCKET NUMBER: 31608-20001.20
13     TELECOMMUNICATION INFORMATION:
14     TELEPHONE: (650) 813-5600
15     TELEFAX: (650) 494-0792
16     TELEX: 706141
17     INFORMATION FOR SEQ ID NO: 4:
18     SEQUENCE CHARACTERISTICS:
19     LENGTH: 450 base pairs
20     TYPE: nucleic acid
21     STRANDEDNESS: double
22     TOPOLOGY: linear
23     FEATURE:
24     NAME/KEY: CDS
25     LOCATION: 1..450
26     US-08-862-124-4

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Query Match	39.2%	Score 359.4	DB 3	Length 450
Best Local Similarity	99.7%	Pred. No. 7.8e-93		
Matches 360	Conservative	0	Mismatches 1	Indels 0
				Gaps 0

Qy	70	GATATTGTGTGACGAGCTCCAGGACCCTGTCTTTGTCTCCAGGGGAAAAGAGCCACC	125
Db	73	GATATTGTGTGACGAGCTCCAGGACCCTGTCTTTGTCTCCAGGGGAAAAGAGCCACC	132
Qy	130	CTCTCTCGCAGGAGCAGTCAGAGTGTAGTACAGCTTACCTGGTGGTACACAGAGAA	189
Db	133	CTCTCTCGCAGGAGCAGTCAGAGTGTAGTACAGCTTACCTGGTGGTACACAGAGAA	192
Qy	190	CTGTGCGCAGGCTCCAGGCTCTCATTTATGGTGATTCACACAGGGCCACTGGCATGCCA	249
Db	193	CTGTGCGCAGGCTCCAGGCTCTCATTTATGGTGATTCACACAGGGCCACTGGCATGCCA	252
Qy	250	GACAGGTTAGTGGCAGTGGGTCCGGGACAACCTTCCTCACTCAATCAGTAGACCTGGAG	309
Db	253	GACAGGTTAGTGGCAGTGGGTCCGGGACAACCTTCCTCACTCAATCAGTAGACCTGGAG	312
Qy	310	CTCGAAGATTTTGGCAGTGTATTTACGTGACGAGTATGGTGTCACTCAGACACACTCAG	369
Db	313	CTCGAAGATTTTGGCAGTGTATTTACGTGACGAGTATGGTGTCACTCAGACACACTCAG	372
Qy	370	ATCAGCTTTGGCGGAGGAGCCAAAGGTGAGATCAAAACGAATCTGGCTGCACCATCTGTC	429
Db	373	ATCAGCTTTGGCGGAGGAGCCAAAGGTGAGATCAAAACGAATCTGGCTGCACCATCTGTC	432
Qy	430	T	430
Db	433	T	433

RESULT 7  
US-08-487-283A-19  
; Sequence 19, Application US/08487283A  
; Patent No. 6355245

1	APPLICANT:	Evans, Mark J.
2	APPLICANT:	Matteis, Louis A.
3	APPLICANT:	Meiller, Eileen Elliott
4	APPLICANT:	Mye, Steven H.
5	APPLICANT:	Rollins, Scott
6	APPLICANT:	Rother, Russell P.
7	APPLICANT:	Springshorn, Jeremy P.
8	APPLICANT:	Scinto, Stephen P.

APPLICANT: Thomas, Thomas C.  
APPLICANT: Wilkins, James A.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT  
OF INFLAMMATORY DISEASES  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Seth A. Fidel  
STREET: 25 Science Park (Alexion)  
CITY: New Haven  
STATE: Connecticut  
COUNTRY: USA  
ZIP: 06511  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.4mb storage  
COMPUTER: Macintosh Celis 610  
OPERATING SYSTEM: System 7  
SOFTWARE: Wordperfect 3.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,283A  
FILING DATE: June 7, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/236,208  
FILING DATE: 02-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Seth A. Fidel.  
REGISTRATION NUMBER: 38,449  
REFERENCE/DOCKET NUMBER: ALX-152.1 CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (203) 776-1790  
TELEFAX: (203) 772-3655  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 783 base pairs  
TYPE: Nucleic Acid  
STRANDEDNESS: Double  
TOPOLOGY: linear  
MOLECULE TYPE: Other nucleic acid  
DESCRIPTION: N19/8 scrv (His Tagged)  
US-08-487-283A-19

Query Match 37.6%; Score 345.2; DB 3; Length 783;  
Best Local Similarity 69.3%; Pred. No. 1.2e-88;  
Matches 552; Conservative 0; Mismatches 193; Indels 51; Gaps 4;

66 GGGCCATATTGTGTGACGAGCTCTCCAGCACCCCTGTTGTCTCCAGGGGAAAGAC 125  
|||||  
3 GGGCAATATTGTGCTACCCAACTCCAGCTTGTGTGTGCTGTGGGCGAGGGGC 62  
126 CACCTCTCTGCGAGGGCCAGTCAAGTGTAGTAG-----CAGCTACTTAGCTG 176  
|||||  
63 CACCAATCTCTGAGAGCCAGTGAAGTGTATGATATGACAAATAGTTTATGACATG 122  
|||||  
177 GTAACGAGAAAAGCTGGCAGGCTCCAGGCTCTCATCTATGATGATCCACGAGGC 236  
|||||  
123 GTAACGAGAAAAGCTGGCAGGCTCCAGGCTCTCATCTTCTTGATCCAACTAG 182  
|||||  
237 CACTGCAATGCCAGACAGTTCAGTGCAGTGGTCCGGGACAGACTTCACTTCACT 296  
|||||  
183 ATCTGGGGTCCCGCAGGTTCAAGTGCAGTGGTCTAAGACAGACTTCACTTCACT 242  
|||||  
297 CAGTAGCTGAGAGCTGAAGATTTGACAGTATTAATCTGACAGATAGTAGTCACT 356  
|||||  
243 TGATCTGTGAGAGCTGATGATCTGCAACCTATTTCTGTACCA-----AAA 290  
|||||  
357 TCAGACACTCAGATCACTTTCGCGAGAGGACCAAGGTGAGATCAAACTGTGCG 416  
|||||  
291 TATATGAGTTCCGAAACAGCTTGGAGGGGGGACCAAGCTGGAATAAAGGGA----- 343  
|||||  
417 TGACACATCTGTCTGCGGCTGCGGCTTCCGAGGTGTGATCAAGTGTGAGTGGCT 476  
|||||  
344 -----CCGAGAGTGGCGGCTGCGGCTGCGGAGGATCGGAGAGGCTCTGAGACT 389  
|||||  
477 CCAGGTGACGTGTGAGTCTGGGGGAGGCTGTGTCAGACCTGGAGAGTCTCTGAGACT 536  
|||||

|||||  
Db 390 GGAACCTCAAGCTCGTGAGACTCTGGGGGAGACTTATGTAAGCTTGGAGGCTCCCTAACT 449  
|||||  
Qy 537 CTCTGTGAGAGCTTGAGATTCCTCTTGAAGAGCTTGTGATGCACTGGGTCCGCGAGC 596  
|||||  
Db 450 CTCTGTGAGAGCTTGAGATTCCTCTTGAAGAGCTTGTGATGCACTGGGTCCGCGAGC 509  
|||||  
Qy 597 TCTAGCAAGGGCTGTGAGTGTGGTGCAGTTATATCATATGATGGAAGACCTAAADACTA 656  
|||||  
Db 510 TCCAGAGAAAGAGCTGTGAGTGTGGTGCAGCCATTAATGATATGATGATGATGACTTACTA 569  
|||||  
Qy 657 CGCAGACTCCGTGAGAGGGCCGATTCACCATCTCCAGAGACACTTCCAAAGACGATGTA 716  
|||||  
Db 570 TCCAGACACTGTGAGAGGGCCGATTCACCATCTCCAGAGACATGCAAGAGACCTGTGA 629  
|||||  
Qy 717 TCTAAATGAAACAGCTTGAGACTGAGAGACAGGCTGTCTATTACTGTGTGAGAGATCA 776  
|||||  
Db 630 TCTGCAATGAGCACTGGAAGTCTGAGAGACAGCCTGTATTTCTGTGTAAGAGA--- 686  
|||||  
Qy 777 GAGCTGTGGGTGACTATGACCACTACTAGGCTTGAACGCTGAGGGCAAGGACAC 836  
|||||  
Db 687 -----GACTTATTACTACGGGATTAATGCTCTTCAATGCTGTGGGCAAGGACAC 740  
|||||  
Qy 837 GGTCAACGCTCTCTCA 852  
|||||  
Db 741 GGTCAACGCTCTCTCA 756  
|||||

RESULT 8  
US-08-447-422-15  
Sequence 15, Application US/08447422  
Patent No. 5686579  
GENERAL INFORMATION:  
APPLICANT: SHAMT, Ezekiel Y.  
APPLICANT: ROTHSTEIN, Aser  
TITLE OF INVENTION: Use of Antibody/Antigen Interactions To  
TITLE OF INVENTION: Protect or Modulate Biological Activity  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington, D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/447,422  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION NUMBER:  
APPLICATION NUMBER: US 08/081,410  
FILING DATE: 22-JUN-1993  
APPLICATION NUMBER: US 07/938,505  
FILING DATE: 31-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/205,748  
FILING DATE: 21-JUN-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 17923/102 HYL1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELFX: 904136  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1848 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-447-422-15

Query Match 37.4%; Score 343.6; DB 1; Length 1848;  
Best Local Similarity 72.3%; Pred. No. 4.9e-88;  
Matches 483; Conservative 0; Mismatches 164; Indels 21; Gaps 2;

70 GATATTGTTGAGCAGCTCTCCAGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACC 129  
1 GATATTGTTGAGCAGCTCTCCAGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACC 60  
130 CTCTCTGAGGGCCGAGAGCTTATAGAGCTTATAGAGCTTATAGAGCTTATAGAGGAAA 189  
61 ATGACCTGAGGGCCGAGAGCTTATAGAGCTTATAGAGCTTATAGAGCTTATAGAGGAAA 120  
190 CCTGGCCAGAGCTCCAGAGCTCTCATCTATGAGTATCCAGCAGGGCCACTGGCATGCA 249  
121 TCAGAGTCTCCCGCCAACTCTGAGATTATAGACATCCAACTGGCTTCTGGAGTCCCT 180  
250 GACAGGTTAGTGGCAGTGGGCTCCGAGACAGACTTCACTCTCACTCAGTACAGTGGAG 309  
181 GCTCGCTTCACTGGCAGTGGGCTCTGGAGCTCTTACTCTCTCACTCAGTACAGTGGAG 240  
310 CCTGAAGATTGTCAGTGTATTAAGTGTACAGTGTATAGTGTACAGTGTACAGTGTAC 369  
241 GCTGAAGATTGTCAGTGTATTAAGTGTACAGTGTATAGTGTACAGTGTACAGTGTAC 289  
370 ATCACTTTGGGCGAGGAGCAGAGTGTAGATCAAGATCAAGATCAAGTGTAGTGTAGTGT 427  
290 -TCAGCTTGGAGGGGAGCAGAGTGTAGATCAAGATCAAGATCAAGTGTAGTGTAGTGT 348  
428 -----TCTGGCCGAGGAGGCTTCCGAGTGTAGTGTAGTGTAGTGTAGTGTAGTGT 480  
349 TCCATCTTCCAGAGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 408  
481 GTGAGCTGTGAGAGTCTGGGGGAGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 540  
409 GTCAAGCTGTGAGAGTCTGGGGGAGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 468  
541 TGTGAGCTGTGAGATTCCCTTCAAGACTTGTATGACATCTGGGCTGGGCTGGGCTGTA 600  
469 TGTGAGCTGTGAGATTCCCTTCAAGACTTGTATGACATCTGGGCTGGGCTGGGCTGTA 528  
601 GGCAGAGGGCTGAGAGTGGGCTGAGTATATATATATATATATATATATATATATAT 660  
529 GAGAGGGGCTGAGAGTGGGCTGAGTATATATATATATATATATATATATATATAT 588  
661 GACTCCGTGAGAGGCGGATTCACCATCTCCAGAGACATTCAGAGAGCAGGCTATCTTA 720  
589 GACACAGTGTAGAGGCGGATTCACCATCTCCAGAGACATTCAGAGAGCAGGCTATCT 648  
721 AAAATGAA 728  
649 CAAATGAA 656

RESULT 9  
US-08-862-124-1  
Sequence 1, Application US/08862124  
Patent No. 6207153  
GENERAL INFORMATION:  
APPLICANT: Dan, Michael D.  
APPLICANT: Maitl, Pradip K.  
APPLICANT: Kaplan, Howard A.  
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H1, THAT  
TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE  
TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster LLP

STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/862,124  
FILING DATE: 22-MAY-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Lehman, Susan K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 31608-20001.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 543 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..543  
US-08-862-124-1

Query Match 35.3%; Score 324.4; DB 3; Length 543;  
Best Local Similarity 89.3%; Pred. No. 8.7e-83;  
Matches 349; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

440 GCGGTTCCGAGAGTGTGATGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 499  
152 GGGTTTCT 211  
500 GGGGAGGCGTGTGTCAGCCTGGGAGGCTCTGAGACTCTCTGTCAGCCTCTGATTC 559  
212 GGGGAGGCGTGTGTCAGCCTGGGAGGCTCTGAGACTCTCTGTCAGCCTCTGATTC 271  
560 CTTGAGAGCTTTGCTATGACATGGGCTCCGACAGCTCTGAGCAAGGGCTGAGTGG 619  
272 CTTGAGAGCTTTGCTATGACATGGGCTCCGACAGCTCTGAGCAAGGGCTGAGTGG 331  
620 TGGCAGTTAT 679  
332 TGGCAGTTAT 391  
680 TCACCATCTCCAGAGCCTTCCAGAGCAGGCTGATATATAAATGAAACAGCTGAGAA 739  
392 TCACCATCTCCAGAGCCTTCCAGAGCAGGCTGATATATAAATGAAACAGCTGAGAA 451  
740 CTGAGAGCAGGCTGTCTATTAATCTGTGAGAGATCAGAGCTGTGTGAGTATGACC 799  
452 CTGAGAGCAGGCTGTCTATTAATCTGTGAGAGATCAGAGCTGTGTGAGTATGACC 511  
800 ACTACTACGTTTGAAGCTGTGGGCAAGG 830  
512 ACTACTACGAGTTGAGAGCTGTGGGCAAGG 542

RESULT 10  
US-08-862-124-3/c  
Sequence 3, Application US/08862124  
Patent No. 6207153  
GENERAL INFORMATION:  
APPLICANT: Dan, Michael D.  
APPLICANT: Maitl, Pradip K.

APPLICANT: Kaplan, Howard A.  
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT  
SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE  
TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE  
TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND  
TITLE OF INVENTION: DETECTION OF CANCERS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster LLP  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/862,124  
FILING DATE: 22-MAY-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Lehnhardt, Susan K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 31608-20001.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX: 706141  
INFORMATION FOR SEO ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 543 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-862-124-3

Query Match 35.3%; Score 324.4; DB 3; Length 543;  
Best Local Similarity 89.3%; Pred. No. 8.7e-83;  
Matches 349; Conservative 0; Mismatches 42; Indels 0; Gaps 0;  
QY 440 GGGGTTCCGGAGGTGGATGATCAGGAGGTGGCTCCAGAGGCGAGCTGGAGATCG 499  
DB 392 GGGTTTCTCGTGTCTCTTTTAAGAGGTATCCAGTGTCAAGTGTGAGGTGAGTCTG 333  
QY 500 GGGGAGGCGTGTCCAGCCTGGAGGTCCTGAGACTCTCTGTGAGGCTCTGATTC 559  
DB 332 GGGGAGGCGTGTCCAGCCTGGAGGTCCTGAGACTCTCTGTGAGGCTCTGATTC 273  
QY 560 CCTTCAGAAAGCTTGTCTATGCACTGGGTCCGCGAGCTCTAGGCAAGGGCTGGAGTGG 619  
DB 272 CCTTCAGAAAGCTTGTCTATGCACTGGGTCCGCGAGCTCTAGGCAAGGGCTGGAGTGG 213  
QY 620 TGGCAGTTATATATGATGATGAGAACTAAATACTACGAGACTCCGTAAGAGGCCGAT 679  
DB 212 TGGCAGTTATATATGATGATGAGAACTAAATACTACGAGACTCCGTAAGAGGCCGAT 153  
QY 680 TCACCATCTCCAGAGCACTTCCAGAAACAAGGTGTATCTAAATAATGAACGCTGAGAA 739  
DB 152 TCACCATCTCCAGAGCACTTCCAGAAACAAGGTGTATCTAAATAATGAACGCTGAGAA 93  
QY 740 CTGAGAGACAGCGCTGTCTATTAATGAGAGAGATCAGAGCTGTGGGTGATATGACC 799  
DB 92 CTGAGAGACAGCGCTGTCTATTAATGAGAGAGATCAGAGCTGTGGGTGATATGACC 33  
QY 800 ACTACTACGTTTGAAGCTGTGGGGAAGG 830  
DB 32 ACTACTACGTTTGAAGCTGTGGGGAAGG 2

RESULT 11  
US-09-472-087-61

Sequence 61, Application US/09472087  
Patent No. 6682736  
GENERAL INFORMATION:  
APPLICANT: HANSON, DOUGLAS C.  
APPLICANT: NEVEU, MARK J.  
APPLICANT: MUELLER, EILEEN B.  
APPLICANT: HANKE, JEFFREY H.  
APPLICANT: GILMAN, STEVEN C.  
APPLICANT: DAVIS, C. GEOFFREY  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4  
FILE REFERENCE: ABX-PFI  
CURRENT APPLICATION NUMBER: US/09/472,087  
CURRENT FILING DATE: 1999-12-23  
PRIOR APPLICATION NUMBER: 60/113,647  
PRIOR FILING DATE: 1998-12-23  
NUMBER OF SEQ ID NOS: 147  
SOFTWARE: PatentIn Ver. 2.1  
SEO ID NO 61  
LENGTH: 1413  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-472-087-61

Query Match 34.8%; Score 319.8; DB 4; Length 1413;  
Best Local Similarity 85.2%; Pred. No. 2.8e-81;  
Matches 357; Conservative 0; Mismatches 62; Indels 0; Gaps 0;  
QY 440 GGGGTTCCGGAGGTGGATGATCAGGAGGTGGCTCCAGAGTGCAGCTGTGAGTCTG 499  
DB 20 GGGTTTCTCGTGTCTCTTTTAAGAGGTGTCCAGTGTCAAGTGTGAGCTGGAGTCTG 79  
QY 500 GGGGAGGCGTGTCCAGCCTGGAGGTCCTGAGACTCTCTGTGAGGCTCTGATTC 559  
DB 80 GGGGAGGCGTGTCCAGCCTGGAGGTCCTGAGACTCTCTGTGAGGCTCTGATTC 139  
QY 560 CCTTCAGAAAGCTTGTCTATGCACTGGGTCCGCGAGCTCTAGGCAAGGGCTGGAGTGG 619  
DB 140 CCTTCAGAAAGCTTGTCTATGCACTGGGTCCGCGAGCTCTAGGCAAGGGCTGGAGTGG 199  
QY 620 TGGCAGTTATATATGATGATGAGAACTAAATACTACGAGACTCCGTAAGAGGCCGAT 679  
DB 200 TGGCAGTTATATATGATGATGAGAACTAAATACTACGAGACTCCGTAAGAGGCCGAT 259  
QY 680 TCACCATCTCCAGAGCACTTCCAGAAACAAGGTGTATCTAAATAATGAACGCTGAGAA 739  
DB 260 TCACCATCTCCAGAGCACTTCCAGAAACAAGGTGTATCTGAAATGAACGCTGAGAA 319  
QY 740 CTGAGAGACAGCGCTGTCTATTAATGAGAGAGATCAGAGCTGTGGGTGATATGACC 799  
DB 320 CTGAGAGACAGCGCTGTCTATTAATGAGAGAGATCAGAGCTGTGGGTGATATGACC 379  
QY 800 ACTACTACGTTTGAAGCTGTGGGGAAGGAGCAAGCTGTCTCTCAAGATCC 858  
DB 380 ACTACTACGTTTGAAGCTGTGGGGAAGGAGCAAGCTGTCTCTCAAGATCC 438

RESULT 12  
US-08-591-632-43  
Sequence 43, Application US/08591632  
Patent No. 6261558  
GENERAL INFORMATION:  
APPLICANT: Barbas, Carlos F.  
APPLICANT: Burton, Dennis R.  
APPLICANT: Lerner, Richard A.  
TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL  
TITLE OF INVENTION: ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS  
NUMBER OF SEQUENCES: 92  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: The Scripps Research Institute, Office of  
STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8  
CITY: La Jolla

```

1 STATE: CA
2 COUNTRY: USA
3 ZIP: 92037
4
5 COMPUTER READABLE FORM:
6 MEDIUM TYPE: floppy disk
7 COMPUTER: IBM PC compatible
8 OPERATING SYSTEM: PC-DOS/MS-DOS
9 SOFTWARE: Patent In Release #1.0
10 CURRENT APPLICATION DATA:
11 APPLICATION NUMBER: US/08/591,632
12 FILING DATE: 19-OCT-1994
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: PCT/US94/11907
15 FILING DATE: 19-OCT-1994
16 PRIOR APPLICATION DATA:
17 APPLICATION NUMBER: US 08/308,841
18 FILING DATE: 19-SEP-1994
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: US 08/233,619
21 FILING DATE: 26-APR-1994
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: US 08/139,409
24 FILING DATE: 19-OCT-1993
25 ATTORNEY/AGENT INFORMATION:
26 NAME: Faltling, Thomas
27 REGISTRATION NUMBER: 34,163
28 REFERENCE/DOCKET NUMBER: TERI 332.3
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: (619) 784-2837
31 TELEFAX: (619) 784-9399
32 INFORMATION FOR SEQ ID NO: 43:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 4691 base pairs
35 TYPE: nucleic acid
36 STRANDEDNESS: single
37 TOPOLOGY: circular
38 MOLECULE TYPE: DNA (genomic)
39
40 US-08-591-632-43

```



Db 2788 AAACCTGCGCAGGCTCCAGGCTCTCTCATATGATGATCCAGACAGGCGCACCTGGCATC 2847  
QY 247 CCAGACAGGTTCACTGCGAGTGGTCCGCGACAGACTTCACTCCATCAGTAGACTG 306  
Db 2848 CCAACAGAGTTTCACTGGAGTGGGTCTGGACAGACTTCACTCCATCAGTAGACTG 2907  
QY 307 GAGCTGAAGATTTTGCAGTGTATTACTGTCAAGATGATGATGACTCACTCAGACACT 366  
Db 2908 GAGCTGAAGATTTTGCAGTGTATTACTGTCAAGATGATGATGACTCACTCAGACACT 2961  
QY 367 CAGATCACTTTCGCGAGGAGCAGAGGTGGATCAAGAACTGTCGTCAGACACT 426  
Db 2962 -----TTGCGCAGAGGAGCAGAGGTGAATCAAGAACTGTCGTCAGACACT 3012  
QY 427 GTCT 430  
Db 3013 GTCT 3016

RESULT 14  
US-08-591-632-51  
Sequence 51, Application US/08591632  
Patent No. 6261558  
GENERAL INFORMATION:  
APPLICANT: Barbás, Carlos F.  
APPLICANT: Burton, Dennis R.  
APPLICANT: Lerner, Richard A.  
TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL  
ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS  
NUMBER OF SEQUENCES: 92  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: The Scripps Research Institute, Office of  
Patent Counsel  
STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/591,632  
FILING DATE: 19-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/11907  
FILING DATE: 19-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/308,841  
FILING DATE: 19-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/233,619  
FILING DATE: 26-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/139,409  
FILING DATE: 19-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSRI 332.3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 784-2937  
TELEFAX: (619) 784-9399  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6166 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)

US-08-591-632-51  
Query Match 34.7%; Score 318.4; DB 3; Length 6166;  
Best Local Similarity 88.4%; Pred. No. 1.4e-80;  
Matches 375; Conservative 0; Mismatches 31; Indels 18; Gaps 2;  
QY 7 ATGAAAAAACCGCTATGCGCATTCGAGTTGACATGCTGGTGTGGCTACCGTTGGCAG 66  
Db 4541 ATGAAAAAACCGCTATGCGCATTCGAGTTGACATGCTGGTGTGGCTACCGTTGGCAG 4600  
QY 67 GCGATATATGTTGATGCGCATTCGAGTTGACATGCTGGTGTGGCTACCGTTGGCAG 126  
Db 4601 GCGG---CCGACTCAGCGAGTCTCAGGCACTCTGTCTTCTTCAGGGGAAAGAGCC 4657  
QY 127 ACCCTCTCTGCGAGGCGCAGTCAAGTGTATGATGACATCTTAACCTGTGACAGAG 186  
Db 4658 ACCCTCTCTGCGAGGCGCAGTCAAGTGTATGATGACATCTTAACCTGTGACAGAG 4717  
QY 187 AAACCTGCGCAGGCTCCAGGCTCTCTCATATGATGATCCAGAGGCGCACCTGGCATG 246  
Db 4718 AAACCTGCGCAGGCTCCAGGCTCTCTCATATGATGATCCAGAGGCGCACCTGGCATG 4777  
QY 247 CCAGACAGGTTCACTGCGAGTGGTCCGCGACAGACTTCACTCCATCAGTAGACTG 306  
Db 4778 CCAACAGAGTTTCACTGGAGTGGGTCTGGACAGACTTCACTCCATCAGTAGACTG 4837  
QY 307 GAGCTGAAGATTTTGCAGTGTATTACTGTCAAGATGATGATGACTCACTCAGACACT 366  
Db 4838 GAGCTGAAGATTTTGCAGTGTATTACTGTCAAGATGATGATGACTCACTCAGACACT 4891  
QY 367 CAGATCACTTTCGCGAGGAGCAGAGGTGGATCAAGAACTGTCGTCAGACACT 426  
Db 4892 -----TTGCGCAGAGGAGCAGAGGTGAATCAAGAACTGTCGTCAGACACT 4942  
QY 427 GTCT 430  
Db 4943 GTCT 4946

RESULT 15  
US-09-611-451-51  
Sequence 51, Application US/09611451  
Patent No. 6395275  
GENERAL INFORMATION:  
APPLICANT: Barbás, Carlos F.  
APPLICANT: Burton, Dennis R.  
APPLICANT: Lerner, Richard A.  
TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL  
ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS  
NUMBER OF SEQUENCES: 92  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: The Scripps Research Institute, Office of  
Patent Counsel  
STREET: 10550 No. 6395275th Torrey Pines Road, TPC 8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/611,451  
FILING DATE: 06-JUL-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/591,632  
FILING DATE: 2001-10-29  
APPLICATION NUMBER: US 08/308,841  
FILING DATE: 19-SEP-1994  
APPLICATION NUMBER: US 08/233,619  
FILING DATE: 26-APR-1994



APPLICATION NUMBER: US 08/139,409  
FILING DATE: 19-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSRI 332.3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 784-2937  
TELEFAX: (619) 784-9399  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6166 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 51:  
US-09-611-451-51

Query Match 34.7%; Score 318.4; DB 3; Length 6166;  
Best Local Similarity 88.4%; Pred. No. 1.4e-80;  
Matches 375; Conservative 0; Mismatches 31; Indels 18; Gaps 2;

QY	7	ATGAAAAAACCGCTATCGCGATGCGAGTTGCACTGGCTGTTGGCTACCGGTGGCGCAG	66
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QY	67	GCGATATTGTTGTCAGCAGTCTCCAGGACCCCTGCTTTGTTCTCCAGGGGAAAGAGCC	126
DB	4601	GCGG---CCGAGCTCAGCGCAGTCTCCAGGACCCCTGCTTTGTTCTCCAGGGGAAAGAGCC	4657
QY	127	ACCTCTCTCTGCAAGGCGCAGTCAAGAGTTAGTAGCAGCTACTTAGCTGTGTAACAGCAG	186
DB	4658	ACCTCTCTCTGCAAGGCGCAGTCAAGAGTTAGTAGCAGGCGCTACTTAGCTGTGTAACAGCAG	4717
QY	187	AAACCTGGCCAGGCTCCAGGCTCCCTCATCTATGATGATCCACGAGGCGCACTGGCATG	246
DB	4718	AAACCTGGCCAGGCTCCAGGCTCCCTCATCTATGATGATCCACGAGGCGCACTGGCATG	4777
QY	247	CCAGACAGGTTCACTGAGTGGGTCGGGAGACAGCTTCATCTCAGCATCAGTAGACTG	306
DB	4778	CCAGACAGGTTCACTGAGTGGGTCGGGAGACAGCTTCATCTCAGCATCAGTAGACTG	4837
QY	307	GAGCTTGAAGATTTTGCAGTGTATTACTGTCAAGCAGTATGTAAGTCACTCAGACACT	366
DB	4838	GAGCTTGAAGATTTTGCAGTGTATTACTGTCAAGCAGTATGTAAGTCACTCAGACACT	4891
QY	367	CAGATCACTTTGGGGGAGGAGCAAGAGTGAGATCAAGCAACTGTGGCTGACCATCT	426
DB	4892	-----TTGGGCCAAGGAGCAAGAGTGAGATCAAGCAACTGTGGCTGACCATCT	4942
QY	427	GTCT 430	
DB	4943	GTCT 4946	

Search completed: February 18, 2005, 08:27:53  
Job time : 207 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 18, 2005, 05:58:59 ; Search time 653 Seconds

(without alignments)  
8309.090 Million cell updates/sec

Title: US-09-194-164-13

Perfect score: 918  
Sequence: 1 GAATTCATGAAAAAAGCCG.....ATCACCATTGTAAGCTT 918

Scoring table:  
IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 5384158 seqs, 2955248155 residues

Total number of hits satisfying chosen parameters: 10768316

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
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- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
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- 18: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*
- 19: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*
- 20: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*
- 21: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 22: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	918	100.0	918	10	US-09-782-397-13 Sequence 13, Appl
2	918	100.0	918	17	US-10-651-453-13 Sequence 15, Appl
3	916.4	99.8	918	10	US-09-782-397-15 Sequence 15, Appl
4	916.4	99.8	918	17	US-10-651-453-15 Sequence 15, Appl
5	799.6	87.1	867	10	US-09-782-397-16 Sequence 16, Appl
6	799.6	87.1	867	17	US-10-651-453-16 Sequence 16, Appl
7	798	86.9	867	10	US-09-782-397-18 Sequence 18, Appl
8	798	86.9	867	17	US-10-651-453-18 Sequence 18, Appl
9	395.2	43.1	840	17	US-10-409-938-50 Sequence 20, Appl
10	361	39.3	450	10	US-09-782-397-6 Sequence 6, Appl
11	361	39.3	450	17	US-10-651-453-6 Sequence 6, Appl

12	359.4	39.2	450	10	US-09-782-397-4	Sequence 4, Appl
13	359.4	39.2	450	17	US-10-651-453-4	Sequence 4, Appl
14	337.8	36.8	762	17	US-10-423-847-8	Sequence 8, Appl
15	336.8	36.7	741	17	US-10-423-847-4	Sequence 4, Appl
16	336.8	36.7	756	17	US-10-423-847-1	Sequence 1, Appl
17	336.8	36.7	759	17	US-10-423-847-2	Sequence 2, Appl
18	335.2	36.5	756	17	US-10-423-847-5	Sequence 5, Appl
19	325.4	35.4	543	17	US-10-651-453-1	Sequence 1, Appl
20	325.4	35.4	543	17	US-10-651-453-3	Sequence 3, Appl
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22	324.4	35.3	543	10	US-09-782-397-3	Sequence 3, Appl
23	324.2	35.3	1539	18	US-10-492-729-4	Sequence 4, Appl
24	324.2	35.3	1539	18	US-10-492-729-12	Sequence 12, Appl
25	319.8	34.8	1413	14	US-10-153-382-16	Sequence 16, Appl
26	319.8	34.8	1413	18	US-10-612-497-51	Sequence 61, Appl
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30	315.2	34.3	376	17	US-10-292-088-73	Sequence 73, Appl
31	314.2	34.2	487	17	US-10-395-894-30	Sequence 30, Appl
32	314.2	34.2	487	18	US-10-695-667-30	Sequence 30, Appl
33	314.2	34.2	7576	17	US-10-395-894-6	Sequence 6, Appl
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35	312.6	34.1	420	18	US-10-714-353-3	Sequence 3, Appl
36	312.6	34.1	421	18	US-10-714-353-11	Sequence 11, Appl
37	312	34.0	376	17	US-10-292-088-57	Sequence 57, Appl
38	310.8	33.9	2011	18	US-10-684-109-80	Sequence 80, Appl
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40	310.6	33.8	678	10	US-09-453-234-49	Sequence 49, Appl
41	310.6	33.8	678	10	US-09-453-234-85	Sequence 85, Appl
42	309.4	33.7	1450	17	US-10-291-265-568	Sequence 568, App
43	309.4	33.7	1450	17	US-10-291-265-569	Sequence 569, App
44	309.4	33.7	1450	17	US-10-291-265-570	Sequence 570, App
45	309.4	33.7	1450	17	US-10-291-265-571	Sequence 571, App

#### ALIGNMENTS

RESULT 1  
US-09-782-397-13  
Sequence 13, Application US/09782397 + *As covered*  
Publication No. US20030021779A1  
GENERAL INFORMATION:  
APPLICANT: Dan, Michael D.  
Kaplan, Howard A.  
Mailli, Pradipt K.  
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT  
SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE  
FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND  
DETECTION OF CANCERS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster LLP  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/782,397  
FILING DATE: 13-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/862,124  
FILING DATE: 1997-05-22  
ATTORNEY/AGENT INFORMATION:  
NAME: Lehnhardt, Susan K.



301 AGACTGGAGCCGGAAGATTTGCAAGTATTAATGTCAGAGATAGTAGCTCACTCAG 360  
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RESULT 3  
US-09-782-397-15/c  
Sequence 15, Application US/09782397  
Publication No. US2003002179A1  
GENERAL INFORMATION:  
APPLICANT: Dan, Michael D.  
Macl, Pradip K.  
Kaplan, Howard A.  
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H1, THAT  
SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE  
FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND  
DETECTION OF CANCERS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster LLP  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/782,397

FILING DATE: 13-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/862,124  
FILING DATE: 1997-05-22  
ATTORNEY/AGENT INFORMATION:  
NAME: Lehnhardt, Susan K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 31608-20001.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 918 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-09-782-397-15  
Query Match 99.8%; Score 916.4; DB 10; Length 918;  
Best Local Similarity 99.9%; Pred. No. 1e-273; Mismatches 1; Indels 0; Gaps 0;  
Matches 917; Conserved 0; Mismatches 1; Indels 0; Gaps 0;  
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558 ACACCTCAGATCACTTTGGCGGAGGAGCAAGGTGAGATCAAGAACTGTGGCTGCA 499  
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QY	721	AAATGAACAGCCTGAGAACTGAGAGACAGCGCTGTCTATTACTGTGCGAGAGATCAAGC	780
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; Publication No. US20040091484A1  
; GENERAL INFORMATION:  
; APPLICANT: Dan, Michael D.  
; APPLICANT: Maitl, Pradip K.  
; APPLICANT: Kaplan, Howard A.  
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT SPECIFICALLY DETECT CANCER CELLS,  
; TITLE OF INVENTION: NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PRO  
; TITLE OF INVENTION: DETECTION OF CANCERS  
; FILE REFERENCE: 31608200103  
; CURRENT APPLICATION NUMBER: US/10/651,453  
; CURRENT FILING DATE: 2003-08-29  
; PRIOR APPLICATION NUMBER: US 09/782,397  
; PRIOR FILING DATE: 2001-02-13  
; PRIOR APPLICATION NUMBER: US 08/862,124  
; PRIOR FILING DATE: 1997-05-22  
; PRIOR APPLICATION NUMBER: US 08/657,449  
; PRIOR FILING DATE: 1996-05-22  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 15  
; LENGTH: 918  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-10-651-453-15

Query Match 99.8%; Score 916.4; DB 17; Length 918;  
Best Local Similarity 99.9%; Fred. No. 1e-273;  
Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY	181	CAGCAGAAACCTGGCGCAGGCTCCAGAGCTCTCATCTATGCTGATCCAGCAGGGCCACT	240
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Db	618	AGACTGGAGCCTGAAGATTTTGGCAGTGTATTACTGTACGAGTATGTAGTCACTCCTAG	559

QY	361	ACACCTCAGATCACTTTGGGCGAGGAGCAAGGTGAGATCAAAACCAACTGTGGCTCGA	420
Db	558	ACACCTCAGATCACTTTGGGCGAGGAGCAAGGTGAGATCAAAACCAACTGTGGCTCGA	499
QY	421	CCATCTGTCTCTGGCGGTGGCGGTTCCGAGAGTGGTGAATAGGTGAGGTGGCTCCAG	480
Db	498	CCATCTGTCTCTGGCGGTGGCGGTTCCGAGAGTGGTGAATAGGTGAGGTGGCTCCAG	439
QY	481	GTGCAAGCTGTGTGAGTCTGGGGGGAAGCGGTGATCCAGCCCTGGAGAGTCCCTGAGACTCTCC	540
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QY	601	GGCAAGGGGGCTGTGAGTGGGTGGCGAGTTATATCATATGTATGATGGAAGCACTAATACTACGCA	660
Db	318	GGCAAGGGGGCTGTGAGTGGGTGGCGAGTTATATCATATGTATGGAAGCACTAATACTACGCA	259
QY	661	GACTCCGATGAAGGGCCGATTCACCATCTCCAGAGACCTTCGCAAGAACGCGTGTATCTA	720
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Db	198	AAATATGAAACAGCTGAGAACTGAGGACACGGCTGTCTATTACTGTGTCAGAGATAGAGC	139
QY	781	CTGTGGGTGACTATGACCACTACTACGCGTTTGGACGTCGTGGGGCAAAAGGACACAGGCT	840
Db	138	CTGTGGGTGACTATGACCACTACTACGCGTTTGGACGTCGTGGGGCAAAAGGACACAGGCT	79
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Db	18	CACCATTTAGTGAAGCTT 1	
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US-09-782-397-16			
; Sequence 16, Application US/09782397			
; Publication No. US20030021799A1			
GENERAL INFORMATION:			
APPLICANT: Dan, Michael D.			
Mailli, Pradip K.			
Kaplan, Howard A.			
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT			
SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE			
FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND			
DETECTION OF CANCERS			
NUMBER OF SEQUENCES: 28			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Morrison & Foerster LLP			
STREET: 755 Page Mill Road			
CITY: Palo Alto			
STATE: CA			
COUNTRY: USA			
ZIP: 94304-1018			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: PatentIn Release #1.0, Version #1.30			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/09/782,397			
FILING DATE: 13-Feb-2001			
CLASSIFICATION: <Unknown>			
PRIOR APPLICATION NUMBER: 08/862,124			

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/
/ FILING DATE: 1997-05-22
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lehnhardt, Susan K.
/ REGISTRATION NUMBER: 33,943
/ REFERENCE/DOCKET NUMBER: 31608-20001.20
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650) 813-5600
/ TELEFAX: (650) 494-0792
/ TELEX: 706141
/ INFORMATION FOR SEQ ID NO: 16:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 867 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: join(1..855, 862..867)
/ SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-782-397-16

Query Match      87.1%; Score 799.6; DB 10; Length 867;
Best Local Similarity 94.0%; Pred. No. 1.8e-237;
Matches 863; Conservative 0; Mismatches 4; Indels 51; Gaps 1;

QY 1 GAATTCATGAAAAAACCCTATCGGATCGAGTGGTGGCTGGTTCGCTACCGTT 60
DB 1 GAATTCATGAAAAAACCCTATCGGATCGAGTGGTGGCTGGTTCGCTACCGTT 60
QY 61 GCGCAGCCGATATTGTGTGAAGCAGTCTCCAGGACCCCTGTCTTGTCTCCAGGGAA 120
DB 61 GCGCAGCCGATATTGTGTGAAGCAGTCTCCAGGACCCCTGTCTTGTCTCCAGGGAA 120
QY 121 AAGGCCACCTCTCTCTGCAAGGCGCACTCAGAGTGTATAGACAGCTACTTACCTGGTAC 180
DB 121 AAGGCCACCTCTCTCTGCAAGGCGCACTCAGAGTGTATAGACAGCTACTTACCTGGTAC 180
QY 181 CAGCAGAAACTGGCCAGGCTCCAGGCTCCATCTATGTGTCAGTCCACAGGGGCACT 240
DB 181 CAGCAGAAACTGGCCAGGCTCCAGGCTCCATCTATGTGTCAGTCCACAGGGGCACT 240
QY 241 GGCATGCCAGAGAGTTGAGTGAAGTGGGTCCGGGACAGACTTCACTCACTCACTCACT 300
DB 241 GGCATGCCAGAGAGTTGAGTGAAGTGGGTCCGGGACAGACTTCACTCACTCACTCACT 300
QY 301 AACTGAGACCTGAAAGATTGAGTGAATTAAGTCAAGAGTATGTAAGTCACTCACTCACT 360
DB 301 AACTGAGACCTGAAAGATTGAGTGAATTAAGTCAAGAGTATGTAAGTCACTCACTCACT 360
QY 361 AACTGAGATCACTTTCGCGGAGAGGACCAAGTGAATCAAAAGAACTGTGGTGTGA 420
DB 361 AACTGAGATCACTTTCGCGGAGAGGACCAAGTGAATCAAAAGAACTGTGGTGTGA 420
QY 421 CCATCTGCTCTGCGGCTGCGGCTTCCGAGGTGTGATCAGTGAAGTGGTCCGAC 480
DB 421 TC-----CGACAG 429
QY 481 GTGCACTGTGAGTCTGCGGAGAGCGGTGTCCAGCCTGGAGGTCCCTGAGACTCTCC 540
DB 481 GTGCACTGTGAGTCTGCGGAGAGCGGTGTCCAGCCTGGAGGTCCCTGAGACTCTCC 540
QY 541 TGTGAGCCTCTGAGATTCCTTCAGAACTTTCGTAATGCACTGGGTCCGAGGCTCTGA 600
DB 541 TGTGAGCCTCTGAGATTCCTTCAGAACTTTCGTAATGCACTGGGTCCGAGGCTCTGA 600
QY 601 GCGCAGGCGCTGAGTGTGCGAGTATATCATATGATGAAGCACTAAATACTACGCA 660
DB 601 GCGCAGGCGCTGAGTGTGCGAGTATATCATATGATGAAGCACTAAATACTACGCA 660
QY 661 GACTCCGTGAAGGCGCGATTCACATCTCCAGAGACCTTCCAGAAACGGGTGTATCTA 720
DB 661 GACTCCGTGAAGGCGCGATTCACATCTCCAGAGACCTTCCAGAAACGGGTGTATCTA 720
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QY 721 AAATGAACAGCCTGAGAACTGAGACACGCGTGTATTAATTAATGTCGAGATCAGAGC 780
DB 670 AAATGAACAGCCTGAGAACTGAGACACGCGTGTATTAATTAATGTCGAGATCAGAGC 729
QY 781 CTGTTGGTGAATATGACCACTACTACGTTTGAAGTGTGGGCAAGAGGACCAAGGTC 840
DB 730 CTGTTGGTGAATATGACCACTACTACGTTTGAAGTGTGGGCAAGAGGACCAAGGTC 789
QY 841 ACCGTTCTCTGAGATCCGAAACAAAACCTGATCAGGAGAAAGATGTGAACCTACCAT 900
DB 790 ACCGTTCTCTGAGATCCGAAACAAAACCTGATCAGGAGAAAGATGTGAACCTACCAT 849
QY 901 CACCATTAAGTGAAGCTT 918
DB 850 CACCATTAAGTGAAGCTT 867

RESULT 6
US-10-651-453-16
/ Sequence 16, Application US/10651453
/ Publication No. US20040091484A1
/ GENERAL INFORMATION:
/ APPLICANT: Dan, Michael D.
/ APPLICANT: Maile, Pradip K.
/ APPLICANT: Kaplan, Howard A.
/ TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT SPECIFICALLY DETECT CANCER CELLS.
/ TITLE OF INVENTION: NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PRO:
/ FILE REFERENCE: 316082000103
/ CURRENT APPLICATION NUMBER: US/10/651,453
/ PRIOR FILING DATE: 2003-08-29
/ PRIOR APPLICATION NUMBER: US 09/782,397
/ PRIOR FILING DATE: 2001-02-13
/ PRIOR APPLICATION NUMBER: US 08/862,124
/ PRIOR FILING DATE: 1997-05-22
/ PRIOR APPLICATION NUMBER: US 08/657,449
/ PRIOR FILING DATE: 1996-05-22
/ NUMBER OF SEQ ID NOS: 29
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 16
/ LENGTH: 867
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
/ NAME/KEY: CDS
/ LOCATION: (1)..(855)
/ OTHER INFORMATION:
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (862)..(867)
/ OTHER INFORMATION:
US-10-651-453-16

Query Match      87.1%; Score 799.6; DB 17; Length 867;
Best Local Similarity 94.0%; Pred. No. 1.8e-237;
Matches 863; Conservative 0; Mismatches 4; Indels 51; Gaps 1;

QY 1 GAATTCATGAAAAAACCCTATCGGATCGAGTGGTGGCTGGTTCGCTACCGTT 60
DB 1 GAATTCATGAAAAAACCCTATCGGATCGAGTGGTGGCTGGTTCGCTACCGTT 60
QY 61 GCGCAGCCGATATTGTGTGAAGCAGTCTCCAGGACCCCTGTCTTGTCTCCAGGGAA 120
DB 61 GCGCAGCCGATATTGTGTGAAGCAGTCTCCAGGACCCCTGTCTTGTCTCCAGGGAA 120
QY 121 AAGGCCACCTCTCTCTGCAAGGCGCACTCAGAGTGTATAGAGAGCTACTTACCTGGTAC 180
DB 121 AAGGCCACCTCTCTCTGCAAGGCGCACTCAGAGTGTATAGAGAGCTACTTACCTGGTAC 180
QY 181 CAGCAGAAACTGGCCAGGCTCCAGGCTCCATCTATGTGTCAGTCCACAGGGGCACT 240
DB 181 CAGCAGAAACTGGCCAGGCTCCAGGCTCCATCTATGTGTCAGTCCACAGGGGCACT 240
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QY 241 GGCATGCCAGACAGGTTCACTGGCAGTGGGTCGGGACAGACTTCACTCTACCATCACT 300  
DB 241 GGCATGCCAGACAGGTTCACTGGCAGTGGGTCGGGACAGACTTCACTCTACCATCACT 300  
QY 301 AGACCTGAGACCTGAGAGATTTTGGAGGTATTACTGTCAGACAGATAGTGTAGCTCACTCG 360  
DB 301 AGACCTGAGACCTGAGAGATTTTGGAGGTATTACTGTCAGACAGATAGTGTAGCTCACTCG 360  
QY 361 ACACCTCAGATCACTTTCGGCGGAGGACCAAGGTGAGATCAAAAGAACTGTGTGCA 420  
DB 361 ACACCTCAGATCACTTTCGGCGGAGGACCAAGGTGAGATCAAAAGAACTGTGTGCA 420  
QY 421 CCATCTGTCTTGGCGGTGGCGGTTCCGAGAGGTGTGATCAGGTGGAGGTGGCTCCGAG 480  
DB 421 TC-----CGAGCAG 429  
QY 481 GTGACAGCTGTGAGAGTCTGGGGGAGCGTGTCTCAGACCTGGAGAGTCCCTGAGACTCTCC 540  
DB 430 GTGACAGCTGTGAGAGTCTGGGGGAGCGTGTCTCAGACCTGGAGAGTCCCTGAGACTCTCC 489  
QY 541 TGTGACAGCTGTGAGATTTCCCTTCAAGAGCTTGTCTATGCACTGGGTCCGCGAGCTCTA 600  
DB 490 TGTGACAGCTGTGAGATTTCCCTTCAAGAGCTTGTCTATGCACTGGGTCCGCGAGCTCTA 549  
QY 601 GGCAGAGGAGCTGAGAGTGGGTGGGAGTTATATCATATGATGGAAGCACTAAATATACGCA 660  
DB 550 GGCAGAGGAGCTGAGAGTGGGTGGGAGTTATATCATATGATGGAAGCACTAAATATACGCA 609  
QY 661 GACTCGGTAAAGGAGCGATTTCAACATCTCTCAGAGACATTTCCAAAGAACCGGTATCTA 720  
DB 610 GACTCGGTAAAGGAGCGATTTCAACATCTCTCAGAGACATTTCCAAAGAACCGGTATCTA 669  
QY 721 AAATGAAACAGCTGTGAACTGAGACACGCGTGTCTATTACTGTGCGAGAGATCAAGAC 780  
DB 670 AAATGAAACAGCTGTGAACTGAGACACGCGTGTCTATTACTGTGCGAGAGATCAAGAC 729  
QY 781 CTGTGGGTGATCATATGACCACTAATCGTTTGGAGTCTGGGGCAAAAGGACCAAGGTC 840  
DB 730 CTGTGGGTGATCATATGACCACTAATCGTTTGGAGTCTGGGGCAAAAGGACCAAGGTC 789  
QY 841 ACCGTCTCTCAGAGATCCGAAACAAAACTGATCAGAGGAGAGATCTGAAACATCAACAT 900  
DB 790 ACCGTCTCTCAGAGATCCGAAACAAAACTGATCAGAGGAGAGATCTGAAACATCAACAT 849  
QY 901 CACCATTAAGTGAAGCTT 918  
DB 850 CACCATTAAGTGAAGCTT 867

RESULT 7  
US-09-782-397-18/c  
Sequence 18, Application US/09782397  
Publication No. US20030021779A1  
GENERAL INFORMATION:  
APPLICANT: Dan, Michael D.  
Kaplan, Howard A.  
Mailli, Pradipl K.  
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT  
SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE  
FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND  
DETECTION OF CANCERS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Morrison & Foerster LLP  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/782,397  
FILING DATE: 13-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/862,124  
FILING DATE: 1997-05-22  
ATTORNEY/AGENT INFORMATION:  
NAME: Lehnhardt, Susan K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 31608-20001.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 867 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
US-09-782-397-18  
Query Match 86.9%; Score 798; DB 10; Length 867;  
Best Local Similarity 93.9%; Pred. No. 5.6e-237; Indels 51; Gaps 1;  
Matches 862; Conservative 0; Mismatches 5;  
QY 1 GAATTCATGAAAGAAACCGCTATCGCATGCGAGTTGCACTGGTGTGCTACCGTT 60  
DB 867 GAATTCATGAAAGAAACCGCTATCGCATGCGAGTTGCACTGGTGTGCTACCGTT 808  
QY 61 GCGCAGGCGGATATGTGTGTGACGAGTCTCCAGGCACTCTTGTGTCTCAAGGGA 120  
DB 807 GCGCAGGCGGATATGTGTGTGACGAGTCTCCAGGCACTCTTGTGTCTCAAGGGA 748  
QY 121 AAGGCCACCTCTCCGCGAGGGGCAGTGAGGTATGAGGAGCTACTTACCTGGTAC 180  
DB 747 AAGGCCACCTCTCCGCGAGGGGCAGTGAGGTATGAGGAGCTACTTACCTGGTAC 688  
QY 181 CAGCAAGAACTGGCAGGCTCCAGGCTCTCATCTATGTGATCCACAGGGGCACT 240  
DB 687 CAGCAAGAACTGGCAGGCTCCAGGCTCTCATCTATGTGATCCACAGGGGCACT 628  
QY 241 GGCATGCCAGACAGGTTCACTGGCAGTGGGTCGGGACAGACTTCACTCTACCATCACT 300  
DB 627 GGCATGCCAGACAGGTTCACTGGCAGTGGGTCGGGACAGACTTCACTCTACCATCACT 568  
QY 301 AGACCTGAGACCTGAGAGATTTTGGAGGTATTACTGTCAGACAGATAGTGTAGCTCACTCG 360  
DB 567 AGACCTGAGACCTGAGAGATTTTGGAGGTATTACTGTCAGACAGATAGTGTAGCTCACTCG 508  
QY 361 ACACCTCAGATCACTTTCGGCGGAGGACCAAGGTGAGATCAAAAGAACTGTGTGCA 420  
DB 507 ACACCTCAGATCACTTTCGGCGGAGGACCAAGGTGAGATCAAAAGAACTGTGTGCA 448  
QY 421 CCATCTGTCTTGGCGGTGGCGGTTCCGAGAGGTGTGATCAGGTGGAGGTGGCTCCGAG 480  
DB 447 TC-----CGAGCAG 439  
QY 481 GTGACAGCTGTGAGAGTCTGGGGGAGCGTGTCTCAGACCTGGAGAGTCCCTGAGACTCTCC 540  
DB 438 GTGACAGCTGTGAGAGTCTGGGGGAGCGTGTCTCAGACCTGGAGAGTCCCTGAGACTCTCC 379  
QY 541 TGTGACAGCTGTGAGATTTCCCTTCAAGAGCTTGTCTATGCACTGGGTCCGCGAGCTCTA 600  
DB 378 TGTGACAGCTGTGAGATTTCCCTTCAAGAGCTTGTCTATGCACTGGGTCCGCGAGCTCTA 319  
QY 601 GGCAGAGGAGCTGAGAGTGGGTGGGAGTTATATCATATGATGGAAGCACTAAATATACGCA 660  
DB 318 GGCAGAGGAGCTGAGAGTGGGTGGGAGTTATATCATATGATGGAAGCACTAAATATACGCA 259

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QY 661 GATCCGTAAGGGCCGATTCACCATCTCCAGAGACCTTCCAAGAACAAGGTGATCTTA 720
DB 258 GATCGGTGAAGGGCCGATTCACCATCTCCAGAGACCTTCCAAGAACAAGGTGATCTTA 139
QY 721 AAAATGAACAGCTTGAACTGAGACACGGCTGTCTATTACTGTGCGAGATCAGAC 780
DB 198 AAAATGAACAGCTTGAACTGAGACACGGCTGTCTATTACTGTGCGAGATCAGAC 139
QY 781 CTGTTGGGTGACATATACCACTACTACGGTTTGGAGCTCTGGGGCAAAAGGACCAAGTTC 840
DB 138 CTGTTGGGTGACATATACCACTACTACGGTTTGGTGTCTGGGGCAAAAGGACCAAGTTC 79
QY 841 ACCGTCCTCCAGATCCGAAACAAAATGATCAGGGAAGAAATCTGAACCATCAGAT 900
DB 78 ACCGTCCTCCAGATCCGAAACAAAATGATCAGGGAAGAAATCTGAACCATCAGAT 19
QY 901 CACCATTAAGTGAAGCTT 918
DB 18 CACCATTAAGTGAAGCTT 1

RESULT 8
US-10-651-453-18/c
; Sequence 18, Application US/10651453
; Publication No. US20040091484A1
; GENERAL INFORMATION:
; APPLICANT: Dan, Michael D.
; APPLICANT: Maltl, Pradip K.
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT SPECIFICALLY DETECT CANCER CELLS.
; TITLE OF INVENTION: NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PRO
; FILE REFERENCE: 316082000103
; CURRENT APPLICATION NUMBER: US/10/651,453
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US 09/782,397
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: US 08/862,124
; PRIOR FILING DATE: 1997-05-22
; PRIOR APPLICATION NUMBER: US 08/657,449
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 867
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-651-453-18

Query Match 86.9%; Score 798; DB 17; Length 867;
Best Local Similarity 93.9%; Pred. No. 5,6e-237;
Matches 862; Conservative 0; Mismatches 5; Indels 51; Gaps 1;
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QY 301 AGACTGAGCCGTAAGATTTTTCAGTATTAATCTGTCAGACAGATATGATGATCTCACCTCAG 360
DB 567 AAGCTGAGCCGTAAGATTTTTCAGTATTAATCTGTCAGACAGATATGATGATCTCACCTCAG 508
QY 361 ACACCTCAGATCACTTTCGCGGAGGAGCAAGGTGAGATCAAAAGAACTGTGCTGCA 420
DB 507 ACACCTCAGATCACTTTCGCGGAGGAGCAAGGTGAGATCAAAAGAACTGTGCTGCA 448
QY 421 CCATCTGTCTTGGCGGTGGCGGTCCGAGGTGTGATCAGGTGAGAGTGGCTCCAG 480
DB 447 TC-----CGGACAG 439
QY 481 GTCAGCTGTGAGATCTGGGGGAGGCGTGTCCAGCCTGGAGGCTCCAGACTCTCC 540
DB 438 GTCAGCTGTGAGATCTGGGGGAGGCGTGTCCAGCCTGGAGGCTCCAGACTCTCC 379
QY 541 TGTGAGCCTCTGATTTCCCTTCAGAACTTTGCTATGACATGAGTCCGACAGGCTCTA 600
DB 378 TGTGAGCCTCTGATTTCCCTTCAGAACTTTGCTATGACATGAGTCCGACAGGCTCTA 319
QY 601 GCGAAGGGGCTGAGTGGGTGGCAGTTATATATATGATGAAGCACTAAATATCTAGCA 660
DB 318 GCGAAGGGGCTGAGTGGGTGGCAGTTATATATATGATGAAGCACTAAATATCTAGCA 259
QY 661 GATCCGTGAAGGGCCGATTCACCATCTCCAGAGACCTTCCAAGAACAAGGTGATCTTA 720
DB 258 GATCCGTGAAGGGCCGATTCACCATCTCCAGAGACCTTCCAAGAACAAGGTGATCTTA 199
QY 721 AAAATGAACAGCTTGAACTGAGACACGGCTGTCTATTACTGTGCGAGATCAGAC 780
DB 198 AAAATGAACAGCTTGAACTGAGACACGGCTGTCTATTACTGTGCGAGATCAGAC 139
QY 781 CTGTTGGGTGACTATGACCACTACTACGGTTTGAAGCTGTGGGGCAAAAGGACCAAGTTC 840
DB 138 CTGTTGGGTGACTATGACCACTACTACGGTTTGTGTGTGGGGCAAAAGGACCAAGTTC 79
QY 841 ACCGTCCTCCAGATCCGAAACAAAATGATCAGGGAAGAAATCTGAACCATCAGAT 900
DB 78 ACCGTCCTCCAGATCCGAAACAAAATGATCAGGGAAGAAATCTGAACCATCAGAT 19
QY 901 CACCATTAAGTGAAGCTT 918
DB 18 CACCATTAAGTGAAGCTT 1

RESULT 9
US-10-409-938-20
; Sequence 20, Application US/10409938
; Publication No. US20030219733A1
; GENERAL INFORMATION:
; APPLICANT: Clark et al.
; TITLE OF INVENTION: ANTIBODY GENE TRANSFER AND RECOMBINANT AAV THEREFOR
; FILE REFERENCE: 28335/39282
; CURRENT APPLICATION NUMBER: US/10/409,938
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/371,501
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 840
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(840)
; OTHER INFORMATION:
US-10-409-938-20

Query Match 43.1%; Score 395.2; DB 17; Length 840;
Best Local Similarity 72.1%; Pred. No. 6,1e-112;
Matches 590; Conservative 0; Mismatches 183; Indels 45; Gaps 4;
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QY 56 CCGTTCGCGAGCCGATATTGTGTTGAGCGAGTCCAGGACCCCTGTTGTCTCCAG 115
DB 50 CCAATGGTGTGGCCGATATTGTGCTGACGAGCTCCAGGACCCGTTGTGTGCGAG 109
QY 116 GGGAAAGAGCCACCCCTCTCTGCGAGGCGAGTCAGAGTGTAGTACACTTAAGCCT 175
DB 110 GGGAAAGAGCCACCCCTCTCTGCGAGGCGAGTCAGAGTGTAGTACAGGCGCTCTTAAGCCT 169
QY 176 GGTACAGCAGAAACCTGCGCAGGCTCCAGGCTCTCATCTATGTGTGATCCAGG 235
DB 170 GGTACAGCAGAAACCTGCTGAGGCTCCAGGCTCTCATCTATGTGTGATCCAGG 229
QY 236 CCACTGGCATGCGACAGGTTCAAGTGGAGTGGGCTCGGGAACAATTCACTTCACCA 295
DB 230 CCACTGGCATGCGACAGGTTCAAGTGGAGTGGGCTCGGGAACAATTCACTTCACCA 289
QY 296 TCAGTAGCTGAGCCTGGAAGATTTTGCAGTATTACTGTGACAGTATGTAGCTCAC 355
DB 290 TCGGCGAGACTGAGCCTGGAAGATCTGCGAGTATTAAGTGTGACAGTATGTAGCTCAC 349
QY 356 CTCAGACACCTCAGATCACTTTCGCGGAGGGAACAAGTGGAGATCAAAAGACTGTGG 415
DB 350 C-----GTACACTTTTGGCCAGGCGGACCAAGTGGATCAAAAGTGGTGGCG 397
QY 416 CTGCAACATCTGTCTGCGGCGGTTCGCGAGTGGTGGATGAGTGGAGTGGCT 475
DB 398 -----GTGCTCTGGCGGCGGTTCAGGTGCGGTGCTC-----TAGATCTT 442
QY 476 CCCAGGTGCGAGTGTGAGTCTGCGGAGGCGCTGTGTCAGCCTGGAAGTCCCTGAGAC 535
DB 443 CCCAGGTGCGAGTGTGAGTCTGCGGCGGTGAGGTGGAAGAGCTGGGTCTCGGTGCAAG 502
QY 536 TCTCTGTGCGAGCTCTGAGATTCCTCTTCAAGACTTGTGTATGACTGGTCCGCAAG 595
DB 503 TCTCTGTGCGAGGCTCTGAGAGGACCTTCAGCATGTATGTGTTCACCTGGTCCGCAAG 562
QY 596 CTCCTGAGCAAGGGGCTGAGTGGGTGGGAGTTATCATATGATGGAACACATAATTACT 655
DB 563 CCCCTGGAATGCTCTTGAATGATGGAAGGATCATCCCTATCTTGTGTACATCAACT 622
QY 656 AGCAGACTCCGTGAGAGGCGGATTCACATCTCCAGAGACATTCACAGAAACCGGTGT 715
DB 623 AGCAGAGAGATTCGCGGGGAGAGTCACTTTACCGGAGCAAGCAAGAGCAGCGCT 682
QY 716 ATCTAAAAATGAAACAGCTGAGAACCTGAGACACGCGCTGTCTATTAAGTGTGCAAGATC 775
DB 683 ACATGAGAGTGAACAACCTGCGATCTGAGACACGCGCTGTATTAATGTGCGAGAGAT 742
QY 776 AGAGCTGTGGGTGACTATGACCACTACACAGT-----TTGAGAG 817
DB 743 TTGGCCCCGACTGGGAAGACGATGATTCCTATGATGTAGTGGCCGCGGGGTTCTTTGACT 802
QY 818 TCTGGGCAAGGAGCAAGCTGACCGCTCTCTCAAGA 855
DB 803 TCTGGGCGCAGGAGACCTGTGTCACTGTCTCTCAAGA 840

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RESULT 10
US-09-782-397-6/c
; Sequence 6, Application US/09782397
; Publication No. US20030021779A1
;
; GENERAL INFORMATION:
; APPLICANT: Dan, Michael D.
; Maiti, Pradip K.
; Kadian, Howard A.
;
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT
; SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
; FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
; DETECTION OF CANCERS
;
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Morrison & Foerster LLP
; STREET: 755 Page Mill Road

```

```

; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/782,397
; FILING DATE: 13-Feb-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/862,124
; FILING DATE: 1997-05-22
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 31608-20001.20
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
;
; TELETYPE: 706141
;
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 450 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-782-397-6

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```

Query Match      39.3%; Score 361; DB 10; Length 450;
Best Local Similarity 100.0%; Pred. No. 2,1e-101; Indels 0; Gaps 0;
Matches 361; Conservative 0; Mismatches 0;

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QY 70 GATATTGTGAGCAGATCTCCAGGACCCGTTGTCTCCAGGGAAGAGCCACC 129
DB 378 GATATTGTGAGCAGATCTCCAGGACCCGTTGTCTCCAGGGAAGAGCCACC 319
QY 130 CTCCTCGAGGCGCCAGTCAAGTGTATGACAGCTTAAGCTGTGACAGAGAAA 189
DB 318 CTCCTCGAGGCGCCAGTCAAGTGTATGACAGCTTAAGCTGTGACAGAGAAA 259
QY 190 CTTGGCAGGCTCCAGGCTCTCATCTATGTGTGATCCAGAGGCGCATGGCCA 249
DB 258 CTTGGCAGGCTCCAGGCTCTCATCTATGTGTGATCCAGAGGCGCATGGCCA 199
QY 250 GACAGGTCAAGTGGAGTGGGTCGCGGACAGACTTCACCTCAGCATGATGAG 309
DB 198 GACAGGTCAAGTGGAGTGGGTCGCGGACAGACTTCACCTCAGCATGATGAG 139
QY 310 CTTGAAGATTTTGCAGTGTATTACTGTGACAGATATGATGAGCTCACTTCA 369
DB 138 CTTGAAGATTTTGCAGTGTATTACTGTGACAGATATGATGAGCTCACTTCA 79
QY 370 ATCACTTTGGCGGAGGAGCAAGGTGAGATCAAAAGAACTGTGGCTGACACTGTGC 429
DB 78 ATCACTTTGGCGGAGGAGCAAGGTGAGATCAAAAGAACTGTGGCTGACACTGTGC 19
QY 430 T 430
DB 18 T 18

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```

RESULT 11
US-10-651-453-6/c
; Sequence 6, Application US/10651453
; Publication No. US20040091484A1
;
; GENERAL INFORMATION:
; APPLICANT: Dan, Michael D.
; Maiti, Pradip K.

```

```
APPLICANT: Kaplan, Howard A.
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT SPECIFICALLY DETECT CANCER CELLS,
NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PRO
FILE REFERENCE: 316082000103
CURRENT FILING DATE: 2003-08-29
PRIORITY FILING DATE: 2001-02-13
PRIORITY FILING DATE: 1997-05-22
PRIORITY FILING DATE: 1996-05-22
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 450
TYPE: DNA
ORGANISM: Homo Sapiens
US-10-651-453-6

Query Match      39.3%; Score 361; DB 17; Length 450;
Best Local Similarity 100.0%; Pred. No. 2,1e-101;
Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 GATATTGTTGACGAGCTCTCCAGGACCCCTGTTCTTGTCTCCAGGGGAAAGGCCACC 129
DB 378 GATATTGTTGACGAGCTCTCCAGGACCCCTGTTCTTGTCTCCAGGGGAAAGGCCACC 319
QY 130 CTCTCTGAGGGGCGAGCTCAGAGTGTAGAGCTACTTACCTGCTGACAGAGAA 189
DB 318 CTCTCTGAGGGGCGAGCTCAGAGTGTAGAGCTACTTACCTGCTGACAGAGAA 259
QY 190 CCTGGCCAGGCTCCAGGCTCTCTCATCTATGTCATCCAGGAGGCGCACTGGATGCCA 249
DB 256 CCTGGCCAGGCTCCAGGCTCTCTCATCTATGTCATCCAGGAGGCGCACTGGATGCCA 199
QY 250 GACAGGTTCAAGTGGGAGTGGGTCGGGAGACAACTTCACTCTCAATCATGATGCTGAG 309
DB 198 GACAGGTTCAAGTGGGAGTGGGTCGGGAGACAACTTCACTCTCAATCATGATGCTGAG 139
QY 310 CCTGAAGATTTTGCAGTGTATTACTGTGACAGATATGATGCTCACTCTGACACTCTGAG 369
DB 138 CCTGAAGATTTTGCAGTGTATTACTGTGACAGATATGATGCTCACTCTGACACTCTGAG 79
QY 370 ATCACTTTGGCGGAGGAGCAAGGTGAGATCAACGAAGTGTGGCTGCAACCATCTGTTC 429
DB 78 ATCACTTTGGCGGAGGAGCAAGGTGAGATCAACGAAGTGTGGCTGCAACCATCTGTTC 19
QY 430 T 430
DB 18 T 18

RESULT 12
US-09-782-397-4
; Sequence 4, Application US/09782397
; Publication No. US20030021779A1
; GENERAL INFORMATION:
; APPLICANT: Dan, Michael D.
; Mailel, Pradip K.
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT
; SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
; FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
; DETECTION OF CANCERS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster LLP
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
```

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ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/782,397
FILING DATE: 13-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/862,124
FILING DATE: 1997-05-22
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 31608-20001.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..450
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-782-397-4

Query Match      39.2%; Score 359.4; DB 10; Length 450;
Best Local Similarity 99.7%; Pred. No. 6.5e-101;
Matches 360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 70 GATATTGTTGACGAGCTCTCCAGGACCCCTGTTCTTGTCTCCAGGGGAAAGGCCACC 129
DB 73 GATATTGTTGACGAGCTCTCCAGGACCCCTGTTCTTGTCTCCAGGGGAAAGGCCACC 132
QY 130 CTCTCTGAGGGGCGAGCTCAGAGTGTAGAGCTACTTACCTGCTGACAGAGAA 189
DB 133 CTCTCTGAGGGGCGAGCTCAGAGTGTAGAGCTACTTACCTGCTGACAGAGAA 192
QY 190 CCTGGCCAGGCTCCAGGCTCTCTCATCTATGTCATCCAGGAGGCGCACTGGATGCCA 249
DB 193 CCTGGCCAGGCTCCAGGCTCTCTCATCTATGTCATCCAGGAGGCGCACTGGATGCCA 252
QY 250 GACAGGTTCAAGTGGGAGTGGGTCGGGAGACAACTTCACTCTCAATCATGATGCTGAG 309
DB 253 GACAGGTTCAAGTGGGAGTGGGTCGGGAGACAACTTCACTCTCAATCATGATGCTGAG 312
QY 310 CCTGAAGATTTTGCAGTGTATTACTGTGACAGATATGATGCTCACTCTGACACTCTGAG 369
DB 313 CCTGAAGATTTTGCAGTGTATTACTGTGACAGATATGATGCTCACTCTGACACTCTGAG 372
QY 370 ATCACTTTGGCGGAGGAGCAAGGTGAGATCAACGAAGTGTGGCTGCAACCATCTGTTC 429
DB 373 ATCACTTTGGCGGAGGAGCAAGGTGAGATCAACGAAGTGTGGCTGCAACCATCTGTTC 432
QY 430 T 430
DB 433 T 433

RESULT 13
US-10-651-453-4
; Sequence 4, Application US/10651453
; Publication No. US20040091484A1
; GENERAL INFORMATION:
; APPLICANT: Dan, Michael D.
; Mailel, Pradip K.
```

```
/ APPLICANT: Kaplan, Howard A.
/ TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT SPECIFICALLY DETECT CANCER CELLS,
/ TITLE OF INVENTION: NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PRO
/ TITLE OF INVENTION: DETECTION OF CANCERS
/ FILE REFERENCE: 31608200103
/ CURRENT APPLICATION NUMBER: US/10/651,453
/ PRIOR FILING DATE: 2003-08-29
/ PRIOR APPLICATION NUMBER: US 09/782,397
/ PRIOR FILING DATE: 2001-02-13
/ PRIOR APPLICATION NUMBER: US 08/862,124
/ PRIOR FILING DATE: 1997-05-22
/ PRIOR APPLICATION NUMBER: US 08/657,449
/ PRIOR FILING DATE: 1996-05-22
/ NUMBER OF SEQ ID NOS: 29
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 4
/ LENGTH: 450
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
US-10-651-453-4

Query Match          39.2%; Score 359.4; DB 17; Length 450;
Best Local Similarity 99.7%; Pred. No. 6.5e-101;
Matches 360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 70 GATATTGTGTGACGCGAGTCTCCAGGACCCCTGTTCTTGTCTTCAGGGGAAAGCCACC 129
DB 73 GATATTGTGTGACGCGAGTCTCCAGGACCCCTGTTCTTGTCTTCAGGGGAAAGCCACC 132
QY 130 CTCTCTGAGGGGCGAGTACAGGTGTTAGTACAGCTAGCTGATCCGTGATCCAGAGAA 189
DB 133 CTCTCTGAGGGGCGAGTACAGGTGTTAGTACAGCTAGCTGATCCGTGATCCAGAGAA 192
QY 190 CCTGGCGAGGCTCCAGGCTCTCATCTATGTGTGATCCAGGGGCACTGGCATGCCA 249
DB 193 CCGGCGAGGCTCCAGGCTCTCATCTATGTGTGATCCAGGGGCACTGGCATGCCA 252
QY 250 GACAGGTTGAGTGGCGAGTGGGTCCGGGACAGATTCTACCTCACTACAGTACGAGAG 309
DB 253 GACAGGTTGAGTGGCGAGTGGGTCCGGGACAGATTCTACCTCACTACAGTACGAGAG 312
QY 310 CCTGAAGATTTTGCAGTATTAATCTGTACAGCAGTATGATGATCCTCAGACCTCAG 369
DB 313 CCGAAGATTTTGCAGTATTAATCTGTACAGCAGTATGATGATCCTCAGACCTCAG 372
QY 370 ATCACTTTGGCGGAGGAGCAAGGTGAGATCAAGCAAGCTGGCTGACCATCTGTC 429
DB 373 ATCACTTTGGCGGAGGAGCAAGGTGAGATCAAGCAAGCTGGCTGACCATCTGTC 432
QY 430 T 430
DB 433 T 433

RESULT 14
US-10-423-847-8
/ Sequence 8, Application US/10423847
/ Publication No. US2004009166A1
/ GENERAL INFORMATION:
/ APPLICANT: FILIPULA, DAVID RAY
/ APPLICANT: YANG, KAREN
/ APPLICANT: BASU, AMARITA
/ APPLICANT: WANG, MINGLIANG
/ TITLE OF INVENTION: SINGLE CHAIN ANTIGEN-BINDING POLYPEPTIDES FOR POLYMER
/ FILE REFERENCE: 213, 1180
/ CURRENT APPLICATION NUMBER: US/10/423,847
/ CURRENT FILING DATE: 2003-04-25
/ PRIOR APPLICATION NUMBER: 09/791,578
/ PRIOR FILING DATE: 2001-02-26
/ PRIOR APPLICATION NUMBER: 09/791,540
/ PRIOR FILING DATE: 2001-02-26
/ PRIOR APPLICATION NUMBER: 09/069,842
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/ PRIOR FILING DATE: 1998-04-30
/ PRIOR APPLICATION NUMBER: 60/044,449
/ PRIOR FILING DATE: 1997-04-30
/ PRIOR APPLICATION NUMBER: 60/050,472
/ PRIOR FILING DATE: 1997-06-23
/ PRIOR APPLICATION NUMBER: 60/063,074
/ PRIOR FILING DATE: 1997-10-27
/ PRIOR APPLICATION NUMBER: 60/067,341
/ PRIOR FILING DATE: 1997-12-02
/ NUMBER OF SEQ ID NOS: 45
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 8
/ LENGTH: 762
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(762)
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic 2-7-SC-8
US-10-423-847-8

Query Match          36.8%; Score 337.8; DB 17; Length 762;
Best Local Similarity 69.1%; Pred. No. 3.9e-94;
Matches 541; Conservative 0; Mismatches 197; Indels 45; Gaps 4;

QY 69 GATATTGTGTGACGCGAGTCTCCAGGACCCCTGTTCTTGTCTTCAGGGGAAAGCCACC 128
DB 3 GATATTGTGTGACGCGAGTCTCCAGGACCCCTGTTCTTGTCTTGTGATCCAGAGATCAG 62
QY 129 CCTCTCTGAGGGGCGAGTACAGGTGTTAGTACAGCTAGCTGATCCGTGATCCAGAGAA 188
DB 133 CACTCTGTCGGGGAAGTCAAG--GCAATCAAGAAATTAATTAAGCTGATCAAGCAAA 119
QY 189 ACCCTGCGAGGCTCCAGGCTCTCATCTATGATGATCAACAGGGCCACTGGCATGCC 248
DB 120 ACCAGGAAAGCCCTTAAGCTCTGATCTATGCTCATCACTTTGCAATCAGGGGTCCC 179
QY 249 AGACAGGTTGAGTGGCGAGTGGGTCCGGGACAGATTCTACCTCACCATTAAGTACGAG 308
DB 180 ATCTGAGTTCAGTGGCGAGTGGGTCTGGGACAGATTCTACCTCACCATTAAGTACGAG 239
QY 309 GCTGAAGATTTTGCAGTATTAATCTGTACAGCAGTATGATGATCCTCAGACCTCAG 368
DB 240 GCTGAAGTGTGCACTTAATTAATCTGTACAGTATTAATCTGTACAGTATTAATCTGT 287
QY 369 GATCACTTTGGCGGAGGAGCAAGGTGAGATCAAGCAAGCTGGCTGACCATCTGTC 428
DB 288 GATCACTTTGGCGGAGGAGCAAGGTGAGATCAAGCAAGCTGGCTGACCATCTGTC 330
QY 429 CTCTGGCGGTCGCTTCCGAGTGGGTGATCAAGTGGAGTGGCTCCAGAGTGAAGCT 488
DB 331 -ACTAGTGTGACGCGCAAACTCCGAGTGGGTGATCAAGTGGAGTGAAGCT 389
QY 489 GGTGAAGTCTGGGGGAGGCGGTGTCAGCTGGAGGATCCTGAGACTCTCTGTGACAC 548
DB 390 GGTGAAGTCTGGGGGAGGCGGTGTCAGCTGGAGGATCCTGAGACTCTCTGTGACAC 449
QY 549 CTCTGATTTCCCTTCAGAACTTTGCTATGATCACTGGGTCCGCAAGCTCTTGAAGG 608
DB 450 CTCTGATTTCACTTTGATGATTAATGATCACTGAGTGGGTCCGCAAGCTCTTGAAGG 509
QY 609 GCTGAAGTGGTGGCGAGTATTAATCAATGATGAAGCACTAAATATACAGCACTCCGT 668
DB 510 CCGAAGTGGTCTGATGATCACTTGAATGATGATGATGATGATGATGATGATGATGAT 569
QY 669 GAAGGCGCATTTCACTATCTCCAGAGCACTTCCAAAGCAAGGTGATCTAAATGAA 728
DB 570 GAAGGCGCATTTCACTATCTCCAGAGCACTTCCAAAGCAAGGTGATCTAAATGAA 629
QY 729 CAGCTGAGAACTGAGAGCACGAGTGTATTAATCTGTGAGAGATCAAGAGCTGTGGG 788
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Db 630 CAGTCTGAGAGTACGAGATACGGCCGTATATTACTGTGCGAAAGTCTGACT----- 683  
 QY 789 TGAAGTACCACTACTAGGTTTGAAGTCTGGGGCAAGGACCAAGTCAACCTCTC 848  
 Db 684 -----TAGACCGCGCTCTCTCCCTTACTATGGGGCAAGTACCTGTCAACCTCTC 737  
 QY 849 CTC 851  
 Db 738 CTC 740

## RESULT 15

US-10-423-847-4  
 ; Sequence 4, Application US/10423847  
 ; Publication No. US20040009166A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FILIPULA, DAVID RAY  
 ; APPLICANT: YANG, KAREN  
 ; APPLICANT: BASU, AMARTYA  
 ; APPLICANT: WANG, MAOLIAN  
 ; TITLE OF INVENTION: SINGLE CHAIN ANTIGEN-BINDING POLYPEPTIDES FOR POLYMER  
 ; FILE REFERENCE: 213, 1180  
 ; CURRENT APPLICATION NUMBER: US/10/423,847  
 ; PRIOR FILING DATE: 2003-04-25  
 ; PRIOR APPLICATION NUMBER: 09/791,578  
 ; PRIOR FILING DATE: 2001-02-26  
 ; PRIOR APPLICATION NUMBER: 09/791,540  
 ; PRIOR FILING DATE: 2001-02-26  
 ; PRIOR APPLICATION NUMBER: 09/069,842  
 ; PRIOR FILING DATE: 1998-04-30  
 ; PRIOR APPLICATION NUMBER: 60/044,449  
 ; PRIOR FILING DATE: 1997-04-30  
 ; PRIOR APPLICATION NUMBER: 60/050,472  
 ; PRIOR FILING DATE: 1997-06-23  
 ; PRIOR APPLICATION NUMBER: 60/063,074  
 ; PRIOR FILING DATE: 1997-10-27  
 ; PRIOR APPLICATION NUMBER: 60/067,341  
 ; PRIOR FILING DATE: 1997-12-02  
 ; NUMBER OF SEQ ID NOS: 45  
 ; SOFTWARE: Patencin Ver. 2.1  
 ; SEQ ID NO 4  
 ; LENGTH: 741  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(741)  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic 2-7-SC-4  
 ; US-10-423-847-4

Query Match 36.7%; Score 336.8; DB 17; Length 741;

Best Local Similarity 69.1%; Pred. No. 7.9e-94; Matches 197; Indels 45; Gaps 4;

QY 70 GATATTGTTGACGAGTCTCCAGGACCCCTGCTTTGCTCCAGGGAAAGACCCACC 129  
 Db 1 GACATCCAGATACCAAGTCTCCATCTCTGCTGATCTGTAGGGGACAGATCACCC 60  
 QY 130 CTCTCTGAGAGGCGGAGTCAAGTGTAGTACAGAGTACTTACCTGTGACAGAGAAA 189  
 Db 61 ATCACTTGTGGGCAAGTCAAG---GACATCAGAAAATTAAGCTGTGATCAGCAAAA 117  
 QY 190 CTTGGCAGAGGCTCCAGGCTCTCATCTATGGGATCCACAGGGGCACTGGAGTCCA 249  
 Db 118 CCAAGGAAAGCCCTTAAGTCTCTGATCTATGCTGATCCATCTTGGCAATCAGGGTCCA 177  
 QY 250 GACAGGTTCAAGTGGAGTGGGTCCGGGACAGACTTCACTCCATCAGTACAGTGGAG 309  
 Db 178 TCTCGTTCAAGTGGAGTGGATCTGGGACAGATTTCATCTCACCATCAGAGCTACAG 237

QY 310 CCTGAAGATTTTGCAGTATATTACTGTGACAGTATGGAGTCACTCAGACACTCAG 369  
 Db 238 CCTGAAGATTTTGCAGTATATTACTGTGACAGTATGGAGTCACTCAGACACTCAG 285  
 QY 370 ATCACTTTCGGGAGGAGCCAAAGGTGAGATCAACGAACTGTGCTGACCACTCTGC 429  
 Db 286 TATACCTTTTGGCCAGGGGACCAAGGTGGAATCAAAAGCTCT----- 327  
 QY 430 TCTGCGGTGGCGGTTCCGGAGGTGTGATCAGGTGAGAGTGGCTCCAGGTGACCTG 489  
 Db 328 ACTAGTGTAGCGGCAAAACCCGGAGGTGTGAGAGTGAAGTCAAAAGTGTGACGCTG 387  
 QY 490 GTGAGTCTGGGGGAGGGGTGTGAGTCCAGCTGGAGAGTCCCTGCTGTGAGCC 549  
 Db 388 GTGAGTCTGGGGGAGGGCTGTGATAGAGCCCGGAGGTCTCTGAGACTCTCTGTGCGGC 447  
 QY 550 TCTGATTCCTCTCAGAACTTTGCTATGCACTGGGTCCGCGAGGCTTGAAGAGGG 609  
 Db 448 TCTGATTCACCTTTGATGATTAATGCACTGGGTCCGCGAGCTTCAAGGAAAGGGC 507  
 QY 610 CTGAGTGGGTGGCAGTTATATCATATGATGAGAGCACTAATTAAGTACGAGACTCCGTG 669  
 Db 508 CTGGAATGGGTCTCAGTATCACTTGAATAGTGTGTCATGATGACTATGCGGACTCTGTG 567  
 QY 670 AAGGCCGATTCACCATCTCCAGAGACACTTCCAGAAACAGGTGTATTAATAATGAA 729  
 Db 568 GAGGGCCGATTCACCATCTCCAGAGACAGCGCAAGAACTCCCTGTATCTGAAATGAA 627  
 QY 720 AGCCTGAGAACTGAGAGACAGGCTGTCTATTAAGTGTGAGAGATCAGAGCTGTGGGT 789  
 Db 628 AGCTGAGAGCTGAGAGATACGGCGGTATATTAAGTGTGAGAAAGTCTGTAAGT----- 680  
 QY 790 GACTATGACCACTACTACGTTTGGACGTCTGGGCAAAAGGACCAAGGTCAAGGTCTCC 849  
 Db 681 -----TAGACCGCGCTCTCTCCCTTGAATATGGGGCAAGGATACCTGGTCAAGGTCTCG 735  
 QY 850 TC 851  
 Db 736 TC 737

Search completed: February 18, 2005, 08:38:53  
 Job time : 657 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: February 18, 2005, 08:24:33 ; Search time 25 Seconds

(without alignments)  
7066.159 Million cell updates/sec

Title: US-09-194-164-13

Perfect score: 1713  
Sequence: 1 GAATTCATGAGAAAAAACCAGC.....ATCACCATTATGTAAGCTT 918

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-Q=/cgn2.1/USPTO.spool/US09194164/runat.16022005.122613.6034/app.query.fasta\_1.1095  
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-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdf -LIST=45  
-LOCALIGN=200 -THR.SCORE=PCT -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=PCO -NOM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09194164\_QCGN\_1.1.26 @runat.16022005.122613.6034 -NCPU=6 -ICPU=3  
-NO.WMAP -LARGECQUERY -NEG.SCORES=0 -THREADS=1 -XGAPOP=10 -LONGLOC  
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :  
PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	541.5	31.6	128	2	E36005 Ig heavy chain V r
2	539.5	31.5	128	2	S48797 Ig heavy chain V r
3	537.5	31.4	215	2	A23746 Ig kappa chain V-I
4	534	31.2	109	2	G30607 Ig kappa chain V-I
5	531	31.0	122	2	S31119 Ig heavy chain - h
6	530	30.9	109	2	A30608 Ig kappa chain V-I
7	530	30.9	109	2	B30601 Ig kappa chain V-I
8	529	30.9	109	2	D30601 Ig kappa chain V-I
9	528.5	30.9	108	2	H4151 Ig kappa chain V r
10	527.5	30.8	215	2	JB0242 Ig kappa chain V r
11	527	30.8	109	2	C30601 Ig kappa chain V-I
12	526	30.7	109	2	F30607 Ig kappa chain V-I
13	526	30.7	129	1	K3H04 Ig kappa chain pre
14	525	30.6	123	2	S38493 Ig heavy chain - h

15	525	30.6	129	2	S49532 anti-Sm antibody V
16	524	30.6	109	2	H30601 Ig kappa chain V-I
17	523	30.5	109	1	K3H01 Ig kappa chain V-I
18	522.5	30.5	114	2	S46375 Ig kappa chain V-J
19	522	30.5	109	2	PH0963 Ig kappa chain V r
20	521	30.4	109	2	G30601 Ig kappa chain V-I
21	520	30.4	129	1	K3H01 Ig kappa chain pre
22	518	30.2	108	2	C30608 Ig kappa chain V-I
23	516	30.1	129	2	S46369 Ig kappa chain var
24	516	30.1	134	2	S38643 Ig kappa chain V r
25	515	30.1	107	2	PH0965 Ig kappa chain V r
26	514	30.0	108	2	B30608 Ig kappa chain V-I
27	514	30.0	145	2	S20631 Ig kappa chain - h
28	513	29.9	119	2	F36005 Ig heavy chain V r
29	512	29.9	109	2	F30601 Ig kappa chain V-I
30	510.5	29.8	104	2	PH0964 Ig kappa chain V r
31	510	29.8	109	1	K3H01 Ig kappa chain V-I
32	510	29.8	128	2	S20636 Ig kappa chain V r
33	509	29.7	121	2	G36005 Ig heavy chain V r
34	508	29.7	134	2	S31679 Ig heavy chain V r
35	507.5	29.6	110	2	E30607 Ig kappa chain V-I
36	507.5	29.6	114	2	S46390 Ig heavy chain V r
37	507.5	29.6	147	2	I37780 Ig variable region
38	506	29.5	109	1	K3H01 Ig kappa chain V-I
39	505	29.5	109	2	F4151 Ig kappa chain V r
40	504.5	29.5	122	2	S31117 Ig heavy chain - h
41	504	29.4	132	2	S31603 Ig heavy chain V r
42	503.5	29.4	108	2	E30609 Ig kappa chain V-I
43	503	29.4	130	2	PL0098 Ig heavy chain pre
44	503	29.4	133	2	A49028 Ig heavy chain V-I
45	502.5	29.3	110	2	S44120 Ig kappa chain V-J

## ALIGNMENTS

RESULT 1  
E36005  
Ig heavy chain V region (M72) - human  
C/Species: Homo sapiens (man)  
C/Date: 21-Dec-1990 #sequence\_revision 21-Dec-1990 #text\_change 16-Dec-1998  
C/Accession: E36005  
R/Schroeder Jr., H.W.; Wang, J.Y.  
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990  
A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene  
A/Reference number: A36005; MUID: 90349571; PMID: 2117273  
A/Accession: E36005  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-122 <SCH>  
A/Cross-References: GB:M34030  
C/Genetics:  
A/Gene: GDB:IGH@; IGHDI1  
A/Cross-References: GDB:118731; OMIM:146910  
A/Map position: 14q32.33-14q32.33  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/15-98/Domain: immunoglobulin homology <1MM>

Alignment Scores:  
Pred. No.: 6,876-31  
Score: 541.50 Length: 122  
Percent Similarity: 88.80% Matches: 105  
Best Local Similarity: 84.00% Conservative: 6  
Query Match: 31.61% Mismatches: 11  
DB: 2 Indels: 3  
Gaps: 1

US-09-194-164-13 (1-918) x E36005 (1-122)

QY 478 CAGGTGACGCTGGTGGAGCTGGGGAGCGGTGTCACGCTGGAGAGTCCCTGAGACTC 537  
|||||  
Db 1 GlnValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20  
|||||  
QY 538 TCCTGTGACGCTCTGAGATTCCCTTCAGAAAGCTTGTGTAAGCACTGGGTCCGCAAGCT 597

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Db      21 SerCysAlaIaIaSerGlyPheThrPheSerSerTyrAlaMetHisTyrValArgGlnAla 40
QY      598 CTAGCAAGAGGGCTGAGTGGTGGTGGTGGTATATCATATGATGAGCACTAAATACTAC 657
Db      41 ProGlyLysGlyLeuGlnTyrPvalAlaValIleSerTyrAspGlySerLeuLeuTyr 60
QY      658 GCAGACTCCGTGAGAGGGCCGATTCCACCATCTCCAGAGACATTCCAAGAACACGGTGTAT 717
Db      61 AlaAspSerValIysGlyArgPheThrIleSerArgAspAsnSerIysAsnThrLeuTyr 80
QY      718 CTAATAATGACACGCTGAGAACTGAGAGACAGCGGTGTCTATATCATCTGGAGAGATCAG 777
Db      81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyrTyrCysAlaArgAspArg 100
QY      778 AGCCTGTGGGTACATATGACCACTACTACGTTTGGAGCTGTGGGCAAGAGGACACG 837
Db      101 His-----SerSerSerTyrTyrTyrGlyMetAspValTrrpGlyGlnGlyThrThr 117
QY      838 GTACACGCTCTCTCA 852
Db      118 ValThrValSerSer 122

RESULT 2
S48797
Ig heavy chain V region (anti-Sm, VH3/Dnp4/JH6) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Sep-1998 #text_change 23-Jul-1999
C/Accession: S48797; S26893
R:Nahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A/Description: Molecular characterization of natural human anti-Sm autoantibodies.
A/Reference number: S48797
A/Accession: S48797
A/Molecule type: mRNA
A/Residues: 1-128 <MAH>
A/Cross-references: EMBL:Z46379; NID:G587147; PIDN:CAA86512.1; PID:G1340168
R:Tomlinson, I.M.; Walter, G.; Marks, U.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A/Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A/Reference number: S26885; MUID:93021117; PMID:1404388
A/Accession: S26893
A/Molecule type: DNA
A/Residues: 1-98 <TOM>
A/Cross-references: EMBL:Z12350; NID:G32922; PIDN:CAA78220.1; PID:G32923
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMW>

Alignment Scores:
Pred. No.: 9.51e-31 Length: 128
Score: 539.50 Matches: 105
Percent Similarity: 86.72% Conservative: 6
Best Local Similarity: 82.03% Mismatches: 14
Query Match: 31.49% Indels: 3
DB: 2 Gaps: 1

US-09-194-164-13 (1-918) x S48797 (1-128)
QY      478 CAGGTGAGCTGTGAGTGTGAGGAGGCTGTCCAGCTGGAGTCCCTGAGACTC 537
Db      1 GlnValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20
QY      538 TCTGTGACGCTCTGAGATTCCCTTCAGAGCTTTGCTAGTACAGTGGTCCGCCAGCT 597
Db      21 SerCysAlaIaIaSerGlyPheThrPheSerSerTyrGlyMetHisTyrValArgGlnAla 40
QY      598 CTAGCAAGAGGGCTGAGTGGTGGTGGTGGTATATCATATGATGAGCACTAAATACTAC 657
Db      41 ProGlyLysGlyLeuGlnTyrPvalAlaValIleTrrpTyrAspGlySerAsnTyrTyr 60
QY      658 GCAGACTCCGTGAGAGGGCCGATTCCACCATCTCCAGAGACATTCCAAGAACACGGTGTAT 717

```

```

Db      61 AlaAspSerValIysGlyArgPheThrIleSerArgAspAsnSerIysAsnThrLeuTyr 80
QY      718 CTAATAATGACACGCTGAGAACTGAGAGACAGCGGTGTCTATATCATCTGGAGAGATCAG 777
Db      81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyrTyrCysAlaArgAspAsn 100
QY      778 -----AGCCTGTGGGTACATATGACCACTACTACGTTTGGAGCTGTGGGCAAA 828
Db      101 TyrTyrTyrAspSerSerGlyTyrTyrTyrTyrTyrGlyMetAspValTrrpGlyGln 120
QY      829 GGGACACGCTACACGCTCTCTCA 852
Db      121 GlyThrThrValThrValSerSer 128

RESULT 3
A23746
Ig kappa chain V-III (KAU cold agglutinin) - human
C/Species: Homo sapiens (man)
C/Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C/Accession: A23746
R:Leon, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A/Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunogl
C/Keywords: heterotetramer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMW>

Alignment Scores:
Pred. No.: 1.3e-30 Length: 215
Score: 537.50 Matches: 128
Percent Similarity: 64.68% Conservative: 13
Best Local Similarity: 58.72% Mismatches: 50
Query Match: 31.38% Indels: 27
DB: 2 Gaps: 5

US-09-194-164-13 (1-918) x A23746 (1-215)
QY      70 GATATTGTGTGAGCACTGTCCAGGACCCCTGCTTGTCTCCAGGGGAAAGCCAC 129
Db      1 GlnIleValIleThrGlnSerProAlaThrLeuSerLeuSerProGlyGlnArgAlaThr 20
QY      130 CTCTCTGACAGGGCCAGTCAAGTGTATAGTACAGCTTACTAGCTGTGTACAGCAGAA 189
Db      21 LeuSerGlyGlyAlaSerGlnSerValSerSerAsnTyrLeuAlaTrrpTyrGlnGlnIys 40
QY      190 CTTGCGCAGGCTCCCGAGCTCTCATCTATGATGATGATCCACGAGGCCACTGGCATGCCA 249
Db      41 ProGlyGlnAlaProArgLeuLeuIleTyrAspAlaSerSerArgAlaThrGlyIlePro 60
QY      250 GACAGTTCAGTGGAGAGGGTCCGGGACACACTTCACTCCACCATCAGTAGAGCTGGAG 309
Db      61 AspArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerArgLeuIle 80
QY      310 CTTGAAGATTTTGCAGTATTAATCTAGTCAGCAGTATGAGTACTGACTCCAGACCTTCAG 369
Db      81 ProGlnAspPheAlaValTyrTyrGlyGlnGlnTyrGlySerSerPro----- 96
QY      370 ATCACTTTGGCGGAGGAGCAAGGTGAGATCAAGAACTGTGGCTGCACCATCTGTC 429
Db      97 LeuThrPheGlyGlyGlyThrIleValGlnIleIysArgThrValAlaAlaProSerVal 116
QY      430 TCTGCGGTGGCGGTCCGAGAGGTGTGATCAGTGTGAGAGGTGCTCCAGGTGACGTG 489
Db      117 PheIlePheProProSerAspGlnGlnLeuIysSerGlyThrAlaSerValValGlyLeu 136
QY      490 GTGAGTCTGGGAGGAGCGGTGTCCAGCTGGAGGTCCTGAGACTCTCTGTGACGCC 549
Db      137 Leu----- 137

```

QY 550 TCTGATCCCTTCAGAGCTTGTCTATGCACTG---GTCCGCCAGGCTTACGACAG 606  
 Db 138 AaanaaPhETyProxArgLualalySValGIntPlySValAAspaanaLaleuGInser 157  
 QY 607 GGGCTGAGATGGGTGGCAGTATATATCATGATGAGACCTAAATACCTAGCAGATCC 666  
 Db 158 GtYaanserGInGInserValThrgUGInaPserLyAAspSerThrTy-----Ser 175  
 QY 667 GTGAAGGCCGATTCACATCTCCAGA---GACACTTCCAGAGACGGTGTAT 717  
 Db 176 LeuSerSerThrLeuThrLeuSerLySAlaAserTyGIntlyGInHlelySValTy 193

## RESULT 4

G30607  
 Ig kappa chain V-III region (Kas) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 21-Jan-2000  
 C:Accession: G30607  
 R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjona, M.L.; Fernandez, J.; Carson, D.; Soló  
 J. Immunol. 142, 3158-3163, 1989  
 A:Title: Structural and idiotypic characterization of the L chains of human Igm autoantib  
 A:Reference number: A30601; MUID:89215279; PMID:2496160  
 A:Accession: G30607  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-109 <GON>  
 C:Superfamily: immunoglobulin V region, immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:16-91/Domain: immunoglobulin homology <IMM>

## Alignment Scores:

Pred. No.:	2,35e-30	Length:	109
Score:	534.00	Matches:	104
Percent Similarity:	95.58%	Conservative:	4
Best Local Similarity:	92.04%	Mismatches:	1
Query Match:	31.17%	Indels:	4
DB:	2	Gaps:	1

US-09-194-164-13 (1-918) x G30607 (1-109)

QY 70 GATATTGTGTGACAGCATCTTCAGAGCCTGTCTTGTCTCAGGGGAAAGACCA 129  
 Db 1 AsplleValleuThGInserProGlyThrLeuSerLeuSerProGlyGInuGValaThr 20  
 QY 130 CTCTCTCAGAGGCGCAGTCAAGTGTATGACACTTACCTGTGATCCAGAGAA 189  
 Db 21 LeuSerCybArGAlaSerGInserLeuSerThrTyLeuAlaTriPtyGInGInly 40  
 QY 190 CTTGCCAGGCTCCAGGCTCTCATCTATGTGTCATCCAGGCGCATGGCA 249  
 Db 41 ProGlyGInAlaProArGLeuLeuLeuTyGlyAlaSerSerArGAlaThrGlyValPro 60  
 QY 250 GACAGGTCAGTGGCAGTGGGTCCGAGACAGCTTCATCATCATGATAGTATGAG 309  
 Db 61 AspaGpHeSerGlySerGlySerGlyThrAspHeThrLeuThrLeuSerTrGInu 80  
 QY 310 CCTGAAGATTTGCACTGATATCTGTCAGCAGTATGATGATGATGATGATGAT 369  
 Db 81 ProGluAaPheAlaValTyTyTyGInGInGInTyGlySerSerPro----- 96  
 QY 370 ATCACTTTCGGCGAGGAGCAAGGATGATCAACCA 408  
 Db 97 PheThrPheGlyGlyGlyThrTyValGInuLeuTySAr 109

## RESULT 5

G31119  
 Ig heavy chain - human  
 C:Species: Homo sapiens (man)  
 C:Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 09-Jul-2004  
 C:Accession: G31119  
 R:Raaphorst, F.M.; Timmers, E.; Kentner, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurmar  
 Eur. J. Immunol. 22, 247-251, 1992

A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple  
 A:Reference number: G31104; MUID:92111633; PMID:1730252  
 A:Accession: G31119  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-122 <RAA>  
 A:Cross-references: UNIPROT:Q9UWU1; EMBL:X62970  
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991  
 C:Superfamily: immunoglobulin V region, immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>

## Alignment Scores:

Pred. No.:	3,83e-30	Length:	122
Score:	531.00	Matches:	105
Percent Similarity:	88.80%	Conservative:	6
Best Local Similarity:	84.00%	Mismatches:	11
Query Match:	31.00%	Indels:	3
DB:	2	Gaps:	1

US-09-194-164-13 (1-918) x G31119 (1-122)

QY 478 CAGTGCAGCTGTGAGATCTGGGAGGCGTGTCCAGCCTGGAGGTCCCTGAGACTC 537  
 Db 1 GInValGInleuValGInserGlyGlyValValGInProGlyArGserLeuArGLeu 20  
 QY 538 TCTGTGCAAGCCTGTGATTCCTTCAGAGCTTGTCTATGACCTGAGTGGTCCGAGGCT 597  
 Db 21 SerCybAlaAlaSerGlyPheThrPheSerSerTyGlyMeHleTriPValArGInAla 40  
 QY 598 CTAGGCAAGGCGCTGAGTGGGTGGCAGTATATCATATGATGAGACCTAAATCTAC 657  
 Db 41 ProGlyLySValLeuGIntPValAlaValleSerTyAspGlySerAsnlySerTyTy 60  
 QY 658 GCAAGCTCCGTAAGGCGGATTCACCATCTCCAGAGACCTCCAGAGACGGGTAT 717  
 Db 61 AlaAspSerValLyGlyArGpHeThrLeuSerArGAspAsnSerLyAsnAnThrLeuTy 80  
 QY 718 CTAATAATGAACGCTGAGAACTGAGGACAGCGGCTGTATTAATCTGTGCGAGATCAG 777  
 Db 81 LeuGInMeCAnSerLeuArGAlaGInAspThrAlaValTyTyCybAlaLyAspGly 100  
 QY 778 AGCCTGTGAGTATGACCATCACTACGTTTGACGTTGGGCGCAAGGACACAG 837  
 Db 101 AlaValAlaGly-Leu-----ArgThrThrValThrPheSerGlyAlaLyGlyProAr 118  
 QY 838 GTCAACGCTCTCCT 850  
 Db 118 GSerProSerPro 122

## RESULT 6

A30608  
 Ig kappa chain V-III region (Son) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 09-Jul-2004  
 C:Accession: A30608  
 R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjona, M.L.; Fernandez, J.; Carson, D.; Soló  
 J. Immunol. 142, 3158-3163, 1989  
 A:Title: Structural and idiotypic characterization of the L chains of human Igm autoantib  
 A:Reference number: A30601; MUID:89215279; PMID:2496160  
 A:Accession: A30608  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-109 <GON>  
 A:Cross-references: UNIPROT:Q9UW78  
 C:Superfamily: immunoglobulin V region, immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:16-91/Domain: immunoglobulin homology <IMM>

## Alignment Scores:

Pred. No.:	4,52e-30	Length:	109
Score:	530.00	Matches:	104
Percent Similarity:	95.58%	Conservative:	4

Best Local Similarity: 92.04%  
 Query Match: 30.94%  
 DB: 2 Indels: 4  
 Gaps: 1

US-09-194-164-13 (1-918) x A30608 (1-109)

```

QY 70 GATATTGTTTACCGACAGCTCCAGGACCCCTGTTTCTTCACAGGGGAAAGACCACC 129
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 1 GUILLEVALLeuThrInserProGlyThrLeuSerLeuSerProGlyGluArgAlaThr 20

QY 130 CTCTCCGAGGAGCCAGTCAGAGTGTAGTACAGCTTACCTGAGCTGATACAGAGAAA 189
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 21 LeuSerCyArGAlaSerInserValSerSerSerTyLeuAlaTrpTyrgInGlnIlys 40

QY 190 CCTGGCCAGGCTCCAGGCTCCTCATCTATGATGTCATCCACAGGCGCATGGCATGCCA 249
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 41 ProGlyGlnAlaProArgLeuLeuIleTyrglyAlaSerSerArgAlaThrGlyLePro 60

QY 250 GACAGGTTACAGGCGAGTGGGTCGCGGACAGACTTACCTCACCATCAGTACAGTGAG 309
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 61 AsnArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerArgLeuGlu 80

QY 310 CCTGAAGATTTTGACAGTGTATTACTGTACAGAGTATGAGTACCTCAGACACTCAG 369
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 81 ProGluAspPheAlaValIleTyrrTyrcysGlnGlnIleTyrglySerSerPro----- 96

QY 370 ATCACTTTCCGCGAGGAGCAAGGTGAGATCAACGA 408
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 97 TyrThrPheGlyGlyGlyThrIlyValGluIleIlyAsArg 109

```

## RESULT 7

Ig kappa chain V-III region (Glo) - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 09-Jul-2004  
 C/Accession: B30601  
 R/Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solc  
 J. Immunol. 142, 3158-3163, 1989  
 A>Title: Structural and idiotypic characterization of the L chains of human IgM autoanti  
 A/Reference number: A30601; PMID:89215279; PMID:2496160  
 A/Accession: B30601  
 A>Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-109 <GON>  
 A/Cross-references: UNIPROT:Q9UL78  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F/16-91/Domain: immunoglobulin homology <IMM>

## Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
530.00	95.58%	109	104	4	1	4	1
92.04%	30.94%						

US-09-194-164-13 (1-918) x B30601 (1-109)

```

QY 70 GATATTGTTTACCGACAGCTCCAGGACCCCTGTTTCTTCACAGGGGAAAGACCACC 129
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 1 GUILLEVALLeuThrInserProGlyThrLeuSerLeuSerProGlyGluArgAlaThr 20

QY 130 CTCTCCGAGGAGCCAGTCAGAGTGTAGTACAGCTTACCTGAGCTGATACAGAGAAA 189
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 21 LeuSerCyArGAlaSerInserValSerSerSerTyLeuAlaTrpTyrgInGlnIlys 40

QY 190 CCTGGCCAGGCTCCAGGCTCCTCATCTATGATGTCATCCACAGGCGCATGGCATGCCA 249
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 41 ProGlyGlnAlaProArgLeuLeuIleTyrglyAlaSerSerArgAlaThrGlyLePro 60

QY 250 GACAGGTTACAGGCGAGTGGGTCGCGGACAGACTTACCTCACCATCAGTACAGTGAG 309
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

```

```

DB 61 AsnArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerArgLeuGlu 80
QY 310 CCTGAAGATTTTGACAGTGTATTACTGTACAGAGTATGAGTACCTCAGACACTCAG 369
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 81 ProGluAspPheAlaValIleTyrrTyrcysGlnGlnIleTyrglySerSerPro----- 96

```

QY 370 ATCACTTTCCGCGAGGAGCAAGGTGAGATCAACGA 408

DB 97 LeuThrPheGlyGlnGlyThrIlyValGluIleIlyAsArg 109

## RESULT 8

Ig kappa chain V-III region (Cur) - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 09-Jul-2004  
 C/Accession: D30601  
 R/Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solc  
 J. Immunol. 142, 3158-3163, 1989  
 A>Title: Structural and idiotypic characterization of the L chains of human IgM autoanti  
 A/Reference number: A30601; PMID:89215279; PMID:2496160  
 A/Accession: D30601  
 A>Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-109 <GON>  
 A/Cross-references: UNIPROT:Q9UL78  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F/16-91/Domain: immunoglobulin homology <IMM>

## Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
532.00	95.58%	109	104	4	1	4	1
92.04%	30.88%						

US-09-194-164-13 (1-918) x D30601 (1-109)

```

QY 70 GATATTGTTTACCGACAGCTCCAGGACCCCTGTTTCTTCACAGGGGAAAGACCACC 129
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 1 GUILLEVALLeuThrInserProGlyThrLeuSerLeuSerProGlyGluArgAlaThr 20

QY 130 CTCTCCGAGGAGCCAGTCAGAGTGTAGTACAGCTTACCTGAGCTGATACAGAGAAA 189
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 21 LeuSerCyArGAlaSerInserValSerSerSerTyLeuAlaTrpTyrgInGlnIlys 40

QY 190 CCTGGCCAGGCTCCAGGCTCCTCATCTATGATGTCATCCACAGGCGCATGGCATGCCA 249
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 41 ProGlyGlnAlaProArgLeuLeuIleTyrglyAlaSerSerArgAlaThrGlyLePro 60

QY 250 GACAGGTTACAGGCGAGTGGGTCGCGGACAGACTTACCTCACCATCAGTACAGTGAG 309
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 61 AsnArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerArgLeuGlu 80

QY 310 CCTGAAGATTTTGACAGTGTATTACTGTACAGAGTATGAGTACCTCAGACACTCAG 369
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 81 ProGluAspPheAlaValIleTyrrTyrcysGlnGlnIleTyrglySerSerProArg----- 97

QY 370 ATCACTTTCCGCGAGGAGCAAGGTGAGATCAACGA 408
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 98 ---ThrPheGlyGlnGlyThrIlyValGluIleIlyAsArg 109

```

## RESULT 9

H44151  
 Ig kappa chain V region (UM-15) - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 27-Jun-1994 #sequence\_revision 27-Jun-1994 #text\_change 09-Jul-2004  
 C/Accession: H44151  
 R/Zebedee, S.L.; Barbash II, C.F.; Hom, Y.L.; Gaothien, R.H.; Graff, R.; Degraw, J.; Py  
 Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992  
 A>Title: Human combinatorial antibody libraries to hepatitis B surface antigen.  
 A/Reference number: A44151; PMID:92228746; PMID:1373487

A:Accession: H44151  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-108 <2EB>  
A:Cross-references: UNIPROT:Q9UL78  
A>Note: nucleotide translation not given  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
P:15-90/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 5,78e-30 Length: 108  
Score: 528.50 Matches: 103  
Percent Similarity: 95.50% Conservative: 3  
Best Local Similarity: 92.79% Mismatches: 5  
Query Match: 30.85% Indels: 0  
DB: 2 Gaps: 1

US-09-194-164-13 (1-918) x H44151 (1-108)

```
QY 79 TTGAGCGAGCTTCACGAGCAGCCCTGCTTTGTCTCCAGGGGAAAGACCACTCTCTGC 138
DB 3 LeuThrGlnSerProGlyThrLeuSerLeuSerProGlyGluArgAlaThrLeuSerCys 22
QY 139 AGGCGCAGTCAGAGTGTAGTACGAGCTACTAGCCTGGTACAGAGAACTGGCCAG 198
DB 23 ArgAlaSerGlnSerValSerSerSerValLeuAlaTrpValGlnGlnProGlyGln 42
QY 199 GCTCCAGAGCTCTCATCTATGAGTGATCCACAGGAGCCATGCGACAGAGTTTC 258
DB 43 AlaProGlnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 62
QY 259 AGTGGCAGTGGTCCGGGACAGACTTCACTTCACCTACAGTACAGTGAAGCTGAAGT 318
DB 63 SerGlySerGlySerGlyThrAspPheThrLeuThrLeuSerArgLeuGlnProGlyAsp 82
QY 319 TTGAGTGTATTACTGTACAGAGATGTAGTACCTCAGACACCTCAGATCCTTTC 378
DB 83 PheAlaValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 97
QY 379 GCGGAGGAGCCAGAGTGGAGATCAACGAGACT 411
DB 98 GlyGlyGlyThrLeuValGlnLeuLeuArgThr 108
```

## RESULT 10

IG kappa chain NIG26 precursor - human  
C:Species: Homo sapiens (man)  
C>Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: J02042  
R:Alt, M.A.; Yamaki, S.; Hossein, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.  
submitted to JIPID, November 1998  
A:Description: Structure relationship of kappa type light chains with AL amyloidosis: Mull  
A:Reference number: J02041  
A:Accession: J02042  
A:Molecule type: protein  
A:Residues: 1-215 <ALI>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
P:16-91/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 6,67e-30 Length: 215  
Score: 527.50 Matches: 125  
Percent Similarity: 62.84% Conservative: 12  
Best Local Similarity: 57.34% Mismatches: 54  
Query Match: 30.79% Indels: 27  
DB: 2 Gaps: 6

US-09-194-164-13 (1-918) x J02042 (1-215)

```
QY 70 GATATTGTTGACGAGCTTCACGAGCAGCCCTGCTTTGTCTCCAGGGGAAAGACGACC 129
DB 1 GlnIleValLeuThrGlnSerProGlyThrLeuSerLeuSerProGlyGluArgAlaThr 20
```

```
QY 130 CTCTCTGAGAGGCCAGTACAGATGTATTAGACAGCTACTTACCTGTGATCCAGCAGAA 189
DB 21 LeuSerCysArgAlaSerGlnSerValSerAlaSerValLeuAlaTrpValGlnGlnLeu 40
QY 190 CCTGGCAGAGCTCCAGAGCTCTCATCTATGAGTGCATCCAGGAGCCAGCTGGACCA 249
DB 41 ProGlyGlnAlaProSerLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60
QY 250 GACAGTTGAGTGGAGTGGGTCCGGGACAGACTTCACTTCACATCAGTACAGTGGAG 309
DB 61 AspArgPheSerGlySerGlySerGlyThrAspPheLeuThrLeuSerGlyLeuGln 80
QY 310 CCTGAAGATTTTGCAGTGTATTACTGTACGACGATGTAGTACCTCAGACACTCAG 369
DB 81 ProGluAspPheAlaValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 96
QY 370 ATCAGTTTGGGAGGAGGAGCAGAGTGGAGATCAACGAACTGTGGCTGACCATGTGTC 429
DB 97 TrpThrPheGlyGlnGlyThrValGlnIleValGlnValAlaAlaProSerVal 116
QY 430 TCTGGCGGTGGCGGTCCGAGGTGGATGATGAGTGGAGTGGCTCCAGAGTGCAGCTG 489
DB 117 -----PheIlePheProSerAspGlnGlnLeu 126
QY 490 GTGAGCTCGGGGAGGAGCTGTCCAGCTGGAGAGTCCCTGAGACTCTCTGTGAGCC 549
DB 127 LysSerGlyThrAlaSerValVal -----CysLeuLeu 137
QY 550 TGTGATTCCTCCCTTCAGAGCTTGTGATGACGTG---GTCCGAGAGCTCTAGGCAAG 606
DB 138 AsnAsnPheTrpProGlyGlnAlaValGlnTrpValAlaAspAsnAlaLeuGlnSer 157
QY 607 GGGCTGAGTGGGTGGCTTATCATATGATGAAAGCATTAATACAGCAGACTCC 666
DB 158 GlnAsnSerGlnGlnSerValThrGlnGlnAspSerValAspSerThrTrp-----Ser 175
QY 667 GTGAAGGCGCATTCACCATCTCCAGA---GACACTTCCAAAGAACGAGTGTAT 717
DB 176 LeuSerSerThrLeuThrLeuSerLeuValAspTrpGlnLeuIleValValTrp 193
```

## RESULT 11

IG kappa chain V-III region (Pay) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 09-Jul-2004  
C:Accession: C30601  
R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjouni, M.L.; Fernandez, J.; Carson, D.; Solc  
U. Immunol. 142, 3158-3163, 1989  
A>Title: Structural and idiotypic characterization of the L chains of human IgM autoanti  
A:Reference number: A30601; MUID:89215279; PMID:2496160  
A:Accession: C30601  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-109 <GON>  
A:Cross-references: UNIPROT:Q9UL78  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
P:16-91/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 7,38e-30 Length: 109  
Score: 527.00 Matches: 103  
Percent Similarity: 95.58% Conservative: 5  
Best Local Similarity: 91.15% Mismatches: 1  
Query Match: 30.76% Indels: 4  
DB: 2 Gaps: 1

US-09-194-164-13 (1-918) x C30601 (1-109)

```
QY 70 GATATTGTTGACGAGCTTCACGAGCAGCCCTGCTTTGTCTCCAGGGGAAAGACGACC 129
DB 1 GlnIleValLeuThrGlnSerProGlyThrLeuSerLeuSerProGlyGluArgAlaThr 20
```

```
QY 130 CTCCTCGAGAGCCAGTCAAGATTAGAGCTACTTACCTGTGTAACAGCGAAA 189
|||
Db 21 LeuSerCyArGAlaSerGlnSerValSerSerSerTyrLeuAlaTrpTyrGlnGlnArg 40
190 CCGGCGAGGAGCTCCAGGCTCCCATCTATGAGTCATCCAGGCGGCACTGGCATGCA 249
|||
Db 41 ProGlyGlnAlaProArgLeuLeuLeuIleTyrGlyAlaSerSerArgAlaThrGlyLeuPro 60
250 GACAGGTTCAAGTGGAGTGGGCTCCGGAGACAGACTTCACTTCCATCCATCAGTAGACTGGAG 309
|||
Db 61 AspArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerArgLeuGln 80
310 CCGAAGATTGTTGCACTGATTAATCTGTCCAGCAGTAGTAGTACCTCAGACACTCAG 369
|||
Db 81 ProGluAspPheAlaValTyrTyrCysGlnGlnTyrGlyAlaSerProGln----- 96
370 ATCACTTTCGGCGGAGGAGCAAGGTGAGATCAACGA 408
|||
Db 97 LeuThrPheGlyGlnGlyThrTyrValGluIleLeuValArg 109

RESULT 12
F30607
Ig kappa chain V-II region (Bor) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-Jul-2004
C/Accession: F30607
R/Gon1, F.R.; Chen, P.P.; McGinnis, D.; Arjouni, M.L.; Fernandez, J.; Carson, D.; Solc
J. Immunol. 142, 3158-3163, 1989
A/Title: Structural and idiotypic characterization of the L chains of human Igm autoanti
A/Reference number: A30601, MUID:89215279; PMID:2496160
A/Accession: F30607
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-109 <GON>
A/Cross-references: UNIPROT:Q5UL78
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 8,7e-30 Length: 109
Score: 526.00 Matches: 103
Percent Similarity: 94.69% Conservative: 4
Best Local Similarity: 91.15% Mismatches: 2
Query Match: 30.71% Indels: 1
DB: 2 Gaps: 1

US-09-194-164-13 (1-918) x F30607 (1-109)
QY 70 GATATTGTGTTGACGAGTCTCCAGGACCCCTGTCTTGTCTCCAGGGGAAAGAGCCACC 129
|||
Db 1 GuileValLeuThrGlnSerProGlyThrLeuSerLeuSerProGlyGluArgAlaThr 20
130 CTCCTCGAGAGGCGAGTCAAGATTAGAGCTACTTACCTGTGTAACAGCGAAA 189
|||
Db 21 LeuSerCyArGAlaSerGlnSerValSerSerSerTyrLeuAlaTrpTyrGlnGlnArg 40
190 CCGGCGAGGAGCTCCAGGCTCCCATCTATGAGTCATCCAGGCGGCACTGGCATGCA 249
|||
Db 41 ProGlyGlnAlaProArgLeuLeuLeuIleTyrGlyAlaSerSerArgAlaThrGlyLeuPro 60
250 GACAGGTTCAAGTGGAGTGGGCTCCGGAGACAGACTTCACTTCCATCCATCAGTAGACTGGAG 309
|||
Db 61 AspArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerArgLeuGln 80
310 CCGAAGATTGTTGCACTGATTAATCTGTCCAGCAGTAGTAGTACCTCAGACACTCAG 369
|||
Db 81 ProGluAspPheAlaValTyrTyrCysGlnGlnTyrGlyAlaSerProGln----- 97
370 ATCACTTTCGGCGGAGGAGCAAGGTGAGATCAACGA 408
|||
Db 98 ---ThrPheGlyGlnGlyThrTyrValGluIleLeuValArg 109
```

```
RESULT 13
K3H0HA
Ig kappa chain precursor V-II region (Hab) - human
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C/Accession: P10022
R/kips, T.J.; Tomhave, E.; Chen, P.P.; Carson, D.A.
J. Exp. Med. 167, 840-852, 1988
A/Title: Autoantibody-associated kappa light chain variable region gene expressed in chr
A/Reference number: P10021; MUID:88171307; PMID:3127527
A/Accession: P10022
A/Molecule type: mRNA
A/Residues: 1-129 <KIP>
A/Cross-references: UNIPROT:P18135
C/Comment: The protein is one of the surface immunoglobulin M autoantibodies expressed i
C/Genetics:
A/Gene: GDB:IGKV3
A/Cross-references: GDB:136266
A/Map position: 2p12-2p11
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kai
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1:
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-129/Product: Ig kappa chain V-II region (Hab) #status predicted <MAT>
F:21-117/Region: V segment
F:36-111/Domain: immunoglobulin homology <IMM>
F:44-55/Region: complementarity-determining 1
F:71-77/Region: complementarity-determining 2
F:118-117/Region: complementarity-determining 3
F:118-129/Region: J segment (JK1)
F:43-109/Disulfide bonds: #status predicted

Alignment Scores:
Pred. No.: 8,65e-30 Length: 129
Score: 526.00 Matches: 103
Percent Similarity: 95.58% Conservative: 5
Best Local Similarity: 91.15% Mismatches: 1
Query Match: 30.71% Indels: 4
DB: 1 Gaps: 1

US-09-194-164-13 (1-918) x K3H0HA (1-129)
QY 70 GATATTGTGTTGACGAGTCTCCAGGACCCCTGTCTTGTCTCCAGGGGAAAGAGCCACC 129
|||
Db 21 GuileValLeuThrGlnSerProGlyThrLeuSerLeuSerProGlyGluArgAlaThr 40
130 CTCCTCGAGAGGCGAGTCAAGATTAGAGCTACTTACCTGTGTAACAGCGAAA 189
|||
Db 41 LeuSerCyArGAlaSerGlnSerValSerSerSerTyrLeuAlaTrpTyrGlnGlnArg 60
190 CCGGCGAGGAGCTCCAGGCTCCCATCTATGAGTCATCCAGGCGGCACTGGCATGCA 249
|||
Db 61 ProGlyGlnAlaProArgLeuLeuLeuIleTyrGlyAlaSerSerArgAlaThrGlyLeuPro 80
250 GACAGGTTCAAGTGGAGTGGGCTCCGGAGACAGACTTCACTTCCATCCATCAGTAGACTGGAG 309
|||
Db 81 AspArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerArgLeuGln 100
310 CCGAAGATTGTTGCACTGATTAATCTGTCCAGCAGTAGTAGTACCTCAGACACTCAG 369
|||
Db 101 ProGluAspPheAlaValTyrTyrCysGlnGlnTyrGlyAlaSerProGln----- 117
370 ATCACTTTCGGCGGAGGAGCAAGGTGAGATCAACGA 408
|||
Db 118 ---ThrPheGlyGlnGlyThrTyrValGluIleLeuValArg 129

RESULT 14
S38493
Ig heavy chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
```

C/Accession: S38493  
R.Marks, J.D.; Ouweland, W.H.; Bye, J.M.; Pinnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S  
submitted to the EMBL Data Library, June 1993  
A:Description: Human antibody fragments specific for human blood group antigens from a B  
A:Reference number: S38488  
A:Accession: S38493  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-123 <MAR>  
A:Cross-References: EMBL:Z23036; NID:g414033; PIDN:CAA80571.1; PID:g414034  
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C:Keywords: heterotrimer; Immunoglobulin  
F:15-98/Domain: Immunoglobulin homology <IMM>

## Alignment Scores:

Pred. No.:	1,02e-29	Length:	123
Score:	525.00	Matches:	104
Percent Similarity:	87.20%	Conservative:	5
Best Local Similarity:	83.20%	Mismatches:	14
Query Match:	30.65%	Indels:	2
DB:	2	Gaps:	1

US-09-194-164-13 (1-918) x S38493 (1-123)

```
OY 478 CAGGTGACGCTGAGTCTGGGGGAGGCGTGCACGCTGGAGGTCCTGAGACTC 537
DB 1 GlnValGlnLeuGlnGlnSerGlyGlyValValGlnProGlyArgSerLeuSerLeu 20
OY 538 TCCTGTGACGCTGATTCCTTCAGAGCTTGTATGACATGAGTCCGACAGCT 597
DB 21 SerCybAlaAlaSerGlyPheSerSerThrAlaMetHisThrValArgGlnAla 40
OY 538 CTAGGCAGAGGGCTGAGTGGGTGAGTATATATATATATATATATATATATAT 657
DB 41 ProGlyLysGlyLeuGlnIleValValIleSerTyraPglSerAsnLysTyrr 60
OY 658 GCAGACTCGGTGAAGGCGGATTCACATCTCCAGAGACACTTCCAGAGACGCTGAT 717
DB 61 AlaAspSerValLysGlyArgPheThrIleSerArgPheAsnSerLysAsnThrLeuTy 80
OY 718 CTAAATGAACAGCTGAGAACTGAGACAGCAGCTGTATTAATGATGAGATCAG 777
DB 81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyrrTyrrCybAlaArgAlaArg 100
OY 778 AGCTGTGGGTGATGATGACCACTACTAGCTTGGAGCTGGGGCAAGGAGACAG 837
DB 101 SerAsnTrpAsnTyrr-----TyrrTyrrMetAspValTrpGlyLysGlyThrThr 118
OY 838 GTACACGCTCTCCTCA 852
DB 119 ValThrValSerSer 123
```

## RESULT 15

S49532  
anti-Sm antibody VL chain (V kappa 3/J kappa 2) - human  
C:Species: Homo sapiens (man)  
C:Date: 01-Feb-1995 #sequence\_revision 12-May-1995 #text\_change 21-Jan-2000  
C:Accession: S49532  
R:Mamoudi, M.; Edwards, J.; Calins, E.; Bell, D.  
submitted to the EMBL Data Library, October 1994  
A:Description: Molecular characterization of natural human anti-Sm autoantibodies.  
A:Reference number: S48797  
A:Accession: S49532  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-129 <MAR>  
A:Cross-References: EMBL:Z46345; NID:g560843; PIDN:CAA86464.1; PID:g560844  
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
F:36-111/Domain: Immunoglobulin homology <IMM>

## Alignment Scores:

Pred. No.:	1,02e-29	Length:	129
Score:	525.00 <td>Matches:</td> <td>103</td>	Matches:	103

Percent Similarity:	94.69%	Conservative:	4
Best Local Similarity: <td>91.15%</td> <td>Mismatches:</td> <td>2</td>	91.15%	Mismatches:	2
Query Match: <td>30.65%</td> <td>Indels:<td>1</td></td>	30.65%	Indels: <td>1</td>	1
DB: <td>2</td> <td>Gaps:<td>4</td></td>	2	Gaps: <td>4</td>	4

US-09-194-164-13 (1-918) x S49532 (1-129)

```
OY 70 GATATTGTTTACCGAGTCTCCAGGACCTGTCTTTGTCTCCAGGGAGAAAGGCCACC 129
DB 21 GlnIleValLeuThrGlnSerProGlyThrLeuSerLeuSerProGlyGlnArgAlaThr 40
OY 130 CTCTCTGAGGGCCAGCAGAGTGTGTATGACAGCTACTTACCTGTCAGACAGAGAA 189
DB 41 LeuSerCybArgAlaSerGlnSerPheSerSerThrLeuAlaTrpTyrrGlnGlnLys 60
OY 190 CTGGCCAGGCTCCAGGCTCTCATCTATGATGATCCAGGAGGAGGAGGAGGATGCA 249
DB 61 ProGlyGlnAlaProArgLeuLeuLeuTyrrGlyAlaSerSerArgAlaThrGlyLeuPro 80
OY 250 GACAGGTTCACTGAGCAGTGGGTCCGGACAGACTTCACTTCACTCAGATCAGTGA 309
DB 81 AsparGpneSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerArgLeuGln 100
OY 310 CCTGAAGATTTTGCAGTGTATTAATGATGATGATGATGATGATGATGATGATGAT 369
DB 101 ProGlnAspPheAlaValTyrrTyrrGlnGlnTyrrGlySerSerProGln----- 117
OY 370 ATCACTTTCGGCGAGGAGCAAGAGGTGAGATCAACGA 408
DB 118 ---ThrPheGlyGlnGlyThrIleLeuGlnIleLeuArg 129
```

Search completed: February 18, 2005, 08:46:50  
Job time : 28 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: February 18, 2005, 07:22:18 ; Search time 109 Seconds

(without alignments) 8625.481 Million cell updates/sec

Title: US-09-194-164-13

Perfect score: 1713  
Sequence: 1 GAATTCATGAAAAAACCGC.....ATCACCATTGTAAGCTT 918

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

MODEL=frame+n2p.model -DEV=xlh  
-O=/cgn2.1/USPTO.spool/US09194164/runat.16022005.122613.6022/app.query.fasta\_1.1095  
-DB=Uniprot\_03 -QFMT=fastaan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blousum62 -TRANS=human0.cdi -LIST=45  
-DOCALLIGN=200 -THR.SCORER=PCT -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pct -NOM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09194164@cgn.1.101 -runat.16022005.122613.6022 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG.SCORER=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Uniprot\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	688	40.2	262	2	Q65Z11
2	555	33.4	236	2	Q6P5S8
3	548	32.0	236	2	Q6P1I8
4	547.5	32.0	235	2	Q6GMV9
5	544.5	31.8	235	2	Q6PJP2
6	530	30.9	109	2	Q9UL78
7	526	30.7	129	1	KV3L_HUMAN
8	523	30.5	109	1	KV3B_HUMAN
9	520	30.4	129	1	KV3M_HUMAN
10	515.5	30.1	613	2	Q8WUK1
11	510	29.8	109	1	KV3D_HUMAN
12	506	29.5	109	1	KV3E_HUMAN
13	506	29.5	240	2	Q65ZC9
14	498.5	29.1	122	1	HV3G_HUMAN
15	497	29.0	109	2	Q9UL86
16	493	28.8	116	2	Q9UL93

17	491	28.7	109	1	KV3G_HUMAN	P04206	homo	sapien
18	486.5	28.4	147	2	Q9Y5O9	Q9Y5O9	homo	sapien
19	484	28.3	108	1	KV3A_HUMAN	P01619	homo	sapien
20	480	28.0	113	2	Q9UL90	Q9UL90	homo	sapien
21	478	27.9	478	2	Q6P181	Q6P181	homo	sapien
22	475	27.7	472	2	Q6N089	Q6N089	homo	sapien
23	473.5	27.6	573	2	Q8WU38	Q8WU38	homo	sapien
24	470	27.4	100	1	KV3C_HUMAN	P01621	homo	sapien
25	468.5	27.3	235	2	Q6GMW0	Q6GMW0	homo	sapien
26	467.5	27.3	606	2	Q6GMV2	Q6GMV2	homo	sapien
27	466	27.2	236	2	Q6PIH7	Q6PIH7	homo	sapien
28	463.5	27.1	122	1	HV3H_HUMAN	P01769	homo	sapien
29	463.5	27.1	544	2	Q6P195	Q6P195	homo	sapien
30	463	27.0	121	1	HV3J_HUMAN	P01771	homo	sapien
31	458.5	26.8	122	2	Q9UL84	Q9UL84	homo	sapien
32	457	26.7	597	2	Q96BB9	Q96BB9	homo	sapien
33	455	26.6	119	1	HV3I_HUMAN	P01770	homo	sapien
34	455	26.6	121	2	Q9UL71	Q9UL71	homo	sapien
35	454	26.5	109	2	Q9UL85	Q9UL85	homo	sapien
36	451	26.3	493	2	Q8NCL6	Q8NCL6	homo	sapien
37	449.5	26.2	128	1	KV3K_HUMAN	P06311	homo	sapien
38	449	26.2	109	1	KV3F_HUMAN	P01624	homo	sapien
39	449	26.2	493	2	Q68CN4	Q68CN4	homo	sapien
40	448.5	26.2	126	1	HV3K_HUMAN	P01772	homo	sapien
41	448	26.2	129	1	KV3L_HUMAN	P04207	homo	sapien
42	445	26.0	464	2	Q6WZ06	Q6WZ06	homo	sapien
43	444	25.9	470	2	Q6PJ44	Q6PJ44	homo	sapien
44	443	25.9	519	2	Q6N092	Q6N092	homo	sapien
45	442	25.8	482	2	Q7Z351	Q7Z351	homo	sapien

# ALIGNMENTS

RESULT 1  
Q65Z11 PRELIMINARY; PRT: 262 AA.  
AC Q65Z11: 25-OCT-2004 (TREMBLrel. 28, Created)  
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)  
DE Anti-HIV-1 reverse transcriptase single-chain variable.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Hybridoma;  
RX MEDLINE=96211469; PubMed=8648670;  
RA Shaheen F., Duan L., Zhu M., Bagasra O., Pomerantz R.J.;  
RT "Targeting human immunodeficiency virus type 1 reverse transcriptase  
RT by intracellular expression of single-chain variable fragments to  
inhibit early stages of the viral life cycle."  
RL J. Virol. 70:3392-3400(1996).  
DR EMBL: U48716; AAB64342.1; -  
DR GO: GO:0003964; F:RNA-directed DNA polymerase activity; IEA.  
DR InterPro: IPR003599; IG.  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003598; IG\_C2.  
DR InterPro: IPR003596; IG\_V.  
DR Pfam: PF00047; IG\_2.  
DR SMART: SM00409; IG\_2.  
DR SMART: SM00408; IG\_C2; 2.  
DR SMART: SM00406; IG\_V; 2.  
DR PROSITE: PS50835; IG\_LIKE; 2.  
KW RNA-directed DNA polymerase.  
SQ SEQUENCE 262 AA; 27842 MM; 7DF20138E53865B4 CRC64;  
Alignment Scores:  
Pred. No.: 4.81e-44 Length: 262  
Score: 688.00 Matches: 142  
Percent Similarity: 67.39% Conservative: 44  
Best Local Similarity: 51.45% Mismatches: 60

Query Match:	40.16%	Indels:	30
DB:	2	Gaps:	6
US-09-194-164-13 (1-918) x Q65211 (1-262)			
QY 70	GATATTGTGTGACGACATCTCCAGGACCCCTGTCTTTGTCTCCAGGGGAAAGCCACC	129	
Db 2	AspillelmetThrInserProAlaThrIleuSerValThrProGlyAspArgValSer	21	
QY 130	CTCCCCGACGGGACGACGAGGTTAAGTACAGACGAACTTAGCGTGTCCAGCAAAA	189	
Db 22	LeuSerYarGalAsaSerGlnSerIle---SerAspPheuHistrPylrGlnGlnlys	40	
QY 190	CTTGACGAGGCTCCAGAGCTCTCTATCTATAGTGCATCCACCAAGGACCTGGATCCA	249	
Db 41	SerHiegluSerProArgLeuLeuIleLysThrAlaSerGlnSerIleSerglyIlePro	60	
QY 250	GACAGGTTCCAGTGGCAGTGGTCCGGGACAGACTTCACTCTACACATCAGTACCTGGAG	308	
Db 61	SerArgPheSerGlySerGlySerGlySerAspPheThrIleuSerIleAsnSerValGlu	80	
QY 310	CCGGAAGATTTTGCAGGTATTACTGTGCAGAGATAGTGGTCAACCTCAGACACTCAG	365	
Db 81	ProGlnuSpAlaGlyValIleTyrTyrCysGlnAsnGlnIleHisSerPhePro-----	96	
QY 370	ATCACTTTCCGCGGAGGAGCCAGAGTGAAGATCAACAGACTGTGGCTGCACATCTGTC	422	
Db 97	LeuThrPheGlyAlaGlyThrLysLeuGlnIleuLysArgAlaSerAlaAlaProThrVal	116	
QY 430	TCT-----GGCGGTGGCGGTCCGAGGTTGGTGA	455	
Db 117	SerIlePheProProSerSerLysLeuGlyProGlyGlyGlySerGlyGlyGlyGly	136	
QY 460	TCAAGTGAAGGTGC-----TCCAGGTGACAGCTGTGTGAGTCTGGGGGA	504	
Db 137	SerGlyGlyGlySerGlnLeuGlyArgSerIleValGlnIleuGlnIleuSerGlyPro	156	
QY 505	GGCGTGTCCAGCTGGAGAGTCCCTGAGACTCTCTGTGTGACAGCTCTGATTCCTCCTTC	564	
Db 157	SerLeuValIysProSerGlnThrIleuSerIleuThrCysSerValIleuGlyAspSerIle	176	
QY 565	AGAAAGCTTGTGTATGACCTGGAGTCCGCGACAGCTCAGGACCAAGGGCTGGAGTGGTGGCA	624	
Db 177	ThrSerGlyTyrTrpAsnTrpIleArgLysPheProGlyAlaLeuAsnLysPheMetGly	196	
QY 625	GTTATATCATATGATGAGGAAGACATMAATACTACGACAGCTCCGTGAAGGCGCATTCAC	684	
Db 197	TyrIleAsnTyrSerGlyAspThr---TyrTyrAsnProSerIleuLysSerArgIleSer	215	
QY 685	ATCCGACGAGACATTCACAGAAACACGAGTATCTMAAATGAAACACCTGAGAAAGAG	744	
Db 216	IleThrIleAspIleSerLysAsnGlnTyrTyrIleuGlnIleuAsnSerValThrThrGlu	233	
QY 745	GACACGAGCTGTCTATTACTGTGCAGAGATCAGACCTGTGTGGTGACTATGACACTAC	804	
Db 236	AspAlaIleAlaThrTyrTyrCysGlyGlyGlyLeuAsnArgThr-----	248	
QY 805	TACGGTTTGACGCTCGGGGCAAAAGGACACAGCTCACCGTCTCTCTCA	852	
Db 249	-----MetAspTyrTrpGlyGlnGlyThrSerValThrValSerSer	262	
RESULT 2			
Q6P5S8	PRELIMINARY;	PRT;	236 AA.
AC Q6P5S8;			
DT 05-JUL-2004 (TREMBLrel. 27, Created)			
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE Hypothetical protein.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TaxID=9606;			

RP SEQUENCE FROM N.A.  
RC TISSUE=Glutaric pool- thyroid;  
EX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;  
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.W., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Ditchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Striplston M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Rana S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
RA Bosak S.A., McWay P.J., McKernan K.O., Malek J.A., Gamarate P.H.,  
RA Richards S., Wolan R.C., Hale S.S., Garcia A.M., Gay L.J., Huliy R.A.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Kravynskii M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RL and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16939-16903(2002).  
RP  
RP SEQUENCE FROM N.A.  
RC TISSUE=Glutaric pool- thyroid;  
RA Strauberg R.,  
RL Submitted (NOV-2003) to the EMBL/Genbank/DBJ databases.  
RL EMBL: BC062704; AAH62704.1; -.  
DR HSP, P01837, 1KCU  
DR InterPro: IPR003599, IG.  
DR InterPro: IPR007110, IG-like.  
DR InterPro: IPR003597, IG\_c1.  
DR InterPro: IPR003006, IG\_MHC.  
DR InterPro: IPR003596, IG\_v.  
DR Pfam: PF07654; Cl-sect; 1.  
DR SMART: SM00409, IG\_2.  
DR SMART: SM00407, IGc1, 1.  
DR SMART: SM00406, IGv, 1.  
DR PROSITE: PS50835, IG\_LIKE, 2.  
DR PROSITE: PS00290, IG\_MHC; UNKOWN\_1.  
KW Hypothetical protein.  
KW SEQUENCE 236 AA; 25773 MW; 955B37BBB4FF5F27 CMC64;  
  
Alignment Scores:  
Pred. No.: 6,66e-34 Length: 236  
Score: 555.00 Matches: 126  
Percent Similarity: 66.06% Conservative: 18  
Best local Similarity: 57.80% Mismatches: 48  
Query Match: 32.40% Indels: 26  
DB: 2 Gaps: 6  
  
US-09-194-164-13 (1-918) x Q6P58 (1-236)  
QY GATATTGTGTGTCAGCAGCTCTCCAGGACCCCTGTTGTCTCCAGGGGAAGACCACC 129  
DB :::: 21 GtalleValleuthrclnserprogllyhrlseuserPheSerProgllyGluArgAlaThr 40  
QY CTCTCTGCGAGGGCGAGCTCAGAGTGTAGTAGACAGTCTTAGCCTGGTACACAGAAA 189  
DB 41 LeuserCyArglalaserGlnThrValPheSerSerHisAlaUAlaTpyrGlnGlnArg 60  
QY CTGCGCGACGGCTCCCGAGGCTCTCATTCATGAGTGATGATCCACGAGGGCGACGCGATCCA 249  
DB 61 ProGlyGlnAlaProArgLeuLeuLeuLeuLeuArgAlaSerSerArgAlaThrGlyLeuPro 80  
QY GACAGGTTACAGTGGCAGTGGGTCCGGACAGACTTCACTCTCACCATCAGTAGACTGAG 309  
DB 81 AspArgPheSerclYserclYserGlyThrArgPheThrLeuThrIleThrArgLeuGlu 100  
QY CCGAAGATTTCAGATGATTACGTCTGACGACAGTATGTTACTCACTCAGACACCTCAG 365

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Db      101 ProGluAepPhaAlaValTyrPheCysGlnGlnTyrGlyThrSer-----ProSer 117
Qy      370 ATCACTTTCGGCGAGGAGCAAGGTGAGATCAACGAACCTGTGCTGCACCATCTGTC 429
Db      118 LeuThrPheGlyGlyGlyThrArgValGluIleValArgThrValAlaIleProSerVal 137
Qy      430 TCTGGCGGCGGCGGCTCCGAGAGTGTGATCAGGTGAGAGTGCTCCAGGTGCAGCTG 489
Db      138 -----PheIlePheProProSerAspGlnGlnLeu 147
Qy      490 GTGAGAGTCTGGGAGGCGGTGCTCAGCTGGAGAGTCCCTGAGACTCTCTGTGACGCC 549
Db      148 LysSerGlyThrAlaSerValVal-----CysLeuLeu 158
Qy      550 TCTGATTCCTCCCTTCAGAGCTTGTCTATGACACTGG---GTCCGCGAGGCTCTAGGCAAG 606
Db      159 AenAenPheTyrProArgIleValAlaValGlnTyrValAlaPheAenAlaLeuGlnSer 178
Qy      607 GGGCTGAGAGTGGGTGACACTTATATCATATGATGAGAGACATTAATCTACGACACTCC 666
Db      179 GlyAenSerGlnGlnSerValThrGlnAenPheSerLysAspSerThrTyr-----Ser 196
Qy      667 GTGAAGGCGCGCATTCACATCTCCAGA---GACACTTCAGAGAACAGCGGTAT 717
Db      197 LeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlnLysHisLysValTyr 214

RESULT 3
Q6PIL8 PRELIMINARY; PRT; 236 AA.
ID      06PIL8
AC      05-JUL-2004 (TREMBLrel. 27, Created)
DT      05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE      Hypochemical protein.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OK      NCBI_TaxID=9606;
RN      (1)
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Struhsberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schaller G.D.,
RA      Altschul S.F., Zeebber B., Buecaw K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Dlacchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.T., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,
RA      Villalón D.K., Muray D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahy J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA      Rodriguez A.C., Gittwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA      Krzysinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
RA      Jones S.J., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences."
RT      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL      (12)
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RA      Struhsberg R.;
RU      Submitted (JUN-2002) to the EMBL/GenBank/DBJ database.
DR      EMBL; BC032451; AAH32451.1; -.
DR      HSSP; P01837; IKC0.
DR      InterPro; IPR003599; IG.
DR      InterPro; IPR007110; IG-like.
DR      InterPro; IPR003597; IG-cl.
DR      InterPro; IPR003006; IG_MHC.

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DR      InterPro; IPR003596; IG_v.
DR      Pfam; PF07654; CI-sec; I.
DR      SMART; SM00409; IG; 2.
DR      SMART; SM00407; IGcl; 1.
DR      SMART; SM00406; IGv; 1.
DR      PROSITE; PSS0835; IG_LIKE; 2.
DR      PROSITE; PSS0290; IG_MHC; UNKNOWN_1.
DR      Hypochemical protein.
SQ      SEQUENCE 236 AA; 25834 MW; 6647A9E77A3C0053 CRC64;

Alignment Scores:
Pred. No.:      2 28e-33      Length:      236
Score:          548.00      Matches:      127
Percent Similarity: 65.28%      Conservative: 14
Best Local Similarity: 58.80%      Mismatches: 49
Query Match:    31.99%      Indels:      26
DB:             2          Gaps:      6

US-09-194-164-13 (1-918) x Q6PIL8 (1-236)
Qy      76 GTGTGACGCACTCTCCAGCACCTGTCTTGTCTCCAGGGGAAAGACCCCTCTCC 135
Db      23 ValLeuThrGlnSerProGlyThrLeuSerLeuSerProGlyGlnArgAlaThrLeuSer 42
Qy      136 TCCAGGCGCCAGTCAAGAGTGTATGACACTTACCTTACCTGTGTTACGACAGAACTGGC 195
Db      43 CysArgAlaSerGlnSerLeuSerSerSerTyrLeuAlaIleTyrGlnGlnLysProGly 62
Qy      196 CAGGCTCCCGAGGCTCCTCATCTATGTGATGATCCACGAGGCGCCAGTGGACGACAGG 255
Db      63 GlnAlaProArgLeuLeuIleTyrGlyValSerSerArgAlaThrGlyIleProAspArg 82
Qy      256 TTCAGTGGCAGTGGGTCCGCGAGACAGACTTCACTTCAACCATGAGTACAGTGGAGCTGAA 315
Db      83 PheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerArgLeuGlnProGlu 102
Qy      316 GATTTCGACGTATATTACTGTACAGCATGTGTAGTCTCACTCCACAGACCTCAGATCACT 375
Db      103 AspPheAlaValTyrTyrCysGlnGlnTyrGlyThrSer-----ArgProIleThr 119
Qy      376 TTCGGCGGAGGAGGACGACGATGAGATCAACGAACGTGGTGCACCATCTGCTTGGC 435
Db      120 PheGlyGlnGlyThrArgLeuAspIleLysArgThrValAlaIleProSerVal----- 137
Qy      436 GGTGGCGGTTCCGAGAGTGTGATCAGGTGAGAGTGCCTCCAGGTGCAGCTGTGGAG 495
Db      138 -----PheIlePheProProSerAspGlnGlnLysSer 149
Qy      496 TTTGGGAGAGGCGTGTGCTCAGCTGGAGAGTCCCTGAGACTCTCTGTGCAGCTTGA 555
Db      150 GlyThrAlaSerValVal-----CysLeuLeuAenAen 160
Qy      556 TTCCTCCCTCAGAGAGCTTGTCTATGACACTGG---GTCCGCGAGGCTCTAGGCAAGGCTG 612
Db      161 PheTyrProArgGlnAlaLysValGlnTyrValAlaPheAenAlaLeuIleSerGlyAen 180
Qy      613 GAGTGGTGGCGACTTATATCATATGATGAGAGACATTAATCTACGACACTCCGGAAG 672
Db      181 SerGlnGlnSerValThrGlnGlnSerLysAspSerThrTyr-----SerLeuSer 198
Qy      673 GGGCATTTCACCATCTCCAGA---GACACTTCAGAGAACAGCGGTAT 717
Db      199 SerThrLeuThrLeuSerLysAlaAspTyrGlnLysHisLysValTyr 214

RESULT 4
Q6GMV9 PRELIMINARY; PRT; 235 AA.
ID      06GMV9
AC      05-JUL-2004 (TREMBLrel. 27, Created)
DT      05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE      Hypochemical protein.
OS      Homo sapiens (Human).

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DR InterPro: IPR007110; Ig-1Ike.  
 DR InterPro: IPR003587; Ig\_C1.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF07654; C1-set; 1.  
 DR SMART: SM00409; Ig; 2.  
 DR SMART: SM00407; IGc1; 1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS00835; IG\_LIKE; 2.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_1.  
 DR Hypothetical protein.  
 SQ SEQUENCE 235 AA; 25520 MW; F33A145A396BA285 CRC64;

## Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score: 4,21e-33	235	544.50	127	15	27	6
Percent Similarity: 65.14%		Conservative: 15				
Best Local Similarity: 58.26%		Mismatches: 49				
Query Match: 31.79%		Indels: 27				
DB: 2		Gaps: 6				

US-09-194-164-13 (1-918) x Q6PUF2 (1-235)

QY 70 GATATTGTTGACGAGCTCCAGGACCCGTTGTTGTCACAGGGGAAAGGACCC 129  
 DB 21 GIULIEVALLEUTHINGLINSEPRoAlaThrLeuSerLeuSerProGlyGluArgAlaThr 40  
 QY 130 CTCTCTGACGGGCGCAGTCAGAGTGTAGTACAGCTACTGACCTGAGCAGAGAA 189  
 DB 41 LeuSerCysArgAlaSerGlnLeuAlaSerSerAlaTyrLeuAlaTyrTrpGlnGln 60  
 QY 190 CTGGGCGAGGCTCCAGGCTCTCATCTATGTCATTCACAGGCGCCATGGCATGCCA 249  
 DB 61 ProGlyGlnAlaProArgLeuLeuMetPheGlySerSerArgAlaThrGlyLeuPro 80  
 QY 250 GACAGTTCAGTGGAGGAGTGGTCCGGGAGACCTTCACCTCAGCATGATGATGAG 309  
 DB 81 AsparGlnPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerArgLeuGlu 100  
 QY 310 CCTGAAGATTGTCAGTGTATTACTGTGTCAGCAGTATGTCAGTCACTCAGACCTCAG 369  
 DB 101 ProGluAspPheAlaValTyrTrpCysGlnGlnTyrGlySerSer-----Gln 116  
 QY 370 ATCATCTTTCGGCGGAGGAGCCAGGTGAGATCAACAGAACTGTGGCTGACCATCTGTC 429  
 DB 117 GlyThrPheGlyProGlyThrIleValAspIleLeuValArgThrValAlaAlaProSerVal 136  
 QY 430 TCTGCGGCTGGCGGCTTCCGGAGGTGTGATCAGGTGAGGTGCTCCAGGTGAGCTG 489  
 DB 137 -----PheIlePheProProSerAspGlnGlnLeu 146  
 QY 490 GTGAGTCTGGGGGAGCGGTGTCAGCTGAGAGGTCCTGAGACTCTCTGTGACGCC 549  
 DB 147 LysSerGlyThrAlaSerVal-----CysLeuLeu 157  
 QY 550 TCTGATTCCTCTTCAAGAGCTTTCATGACCTG---GTCCGCGAGGCTCTTAAAGCAAG 606  
 DB 158 AsnAspPheTyrProArgGlnAlaLeuValGlnTyrValAspAsnAlaLeuGlnSer 177  
 QY 607 GGGCTGAGTGGGTCAGATTATCATATGATGAGAGCACTAAATATACAGCAGACTCC 666  
 DB 178 GlnAsnSerGlnGlnSerValThrGlnGlnAspSerLysAspSerThrTyr-----Ser 195  
 QY 667 GTGAAGGCGCAGTTCACATCTCAGAA--GACACTTCCAGAGACAGGCTGAT 717  
 DB 196 LeuSerSerThrLeuThrLeuSerLysAlaSerTyrGlnLysIleLysValTyr 213

## RESULT 6

Q9UL78 PRELIMINARY; PRT; 109 AA.

ID Q9UL78;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Myosin-reactive Immunoglobulin light chain variable region  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OK NCBI\_TaxId=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 fetus";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL, AF035036; AAD56272.1; -.  
 DR PIR: A30601; A30601.  
 DR PIR: A30608; A30608.  
 DR PIR: B30601; B30601.  
 DR PIR: B30607; B30607.  
 DR PIR: C30601; C30601.  
 DR PIR: C30607; C30607.  
 DR PIR: C30608; C30608.  
 DR PIR: D30601; D30601.  
 DR PIR: D30607; D30607.  
 DR PIR: D30608; D30608.  
 DR PIR: F30607; F30607.  
 DR PIR: F30608; F30608.  
 DR PIR: G30601; G30601.  
 DR PIR: G30608; G30608.  
 DR PIR: H30607; H30607.  
 DR PIR: H30608; H30608.  
 DR PIR: H4151; H4151.  
 DR PIR: I30601; I30601.  
 DR PIR: PH0963; PH0963.  
 DR PIR: PH0964; PH0964.  
 DR PIR: PH0965; PH0965.  
 DR PIR: S33988; S33988.  
 DR PIR: S34096; S34096.  
 DR HSP; P01625; IER3.  
 DR InterPro: IPR007110; Ig-1Ike.  
 DR InterPro: IPR003596; Ig\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 FT NON\_TER 1  
 FT NON\_TER 109  
 SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EB197 CRC64;

## Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score: 4,82e-32	109	530.00	104	4	4	1
Percent Similarity: 95.58%		Conservative: 104				
Best Local Similarity: 92.04%		Mismatches: 4				
Query Match: 30.94%		Indels: 4				
DB: 2		Gaps: 1				

US-09-194-164-13 (1-918) x Q9UL78 (1-109)

QY 70 GATATTGTTGACGAGCTTCAGGACCCGTTGTTGTCACAGGGGAAAGGACCC 129  
 DB 1 GIULIEVALLEUTHINGLINSEPRoAlaThrLeuSerLeuSerProGlyGluArgAlaThr 20  
 QY 130 CTCTCTGACGGGCGCAGTCAGAGTGTAGTACAGCTACTGACCTGAGCAGAGAA 189  
 DB 21 LeuSerCysArgAlaSerGlnLeuAlaSerSerAlaTyrLeuAlaTyrTrpGlnGln 40  
 QY 190 CTGGGCGAGGCTCCAGGCTCTCATCTATGTCATTCACAGGCGCCATGGCATGCCA 249  
 DB 41 ProGlyGlnAlaProArgLeuLeuMetPheGlySerSerArgAlaThrGlyLeuPro 60  
 QY 250 GACAGTTCAGTGGAGGAGTGGTCCGGGAGACCTTCACCTCAGCATGATGAG 309  
 DB 61 AsparGlnPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerArgLeuGlu 80

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QY 310 CCTGAAGATTTCAGGTGATTACTGTGCAGAGTATGTAGTCACTCAGACACCTCAG 369
DB 81 ProgiuaApCysAlaValTyrTyrCysGlnGlnTyrGlySerSerPro----- 96
QY 370 ATCACTTTGGCGGAGGAGCCAGAGTGGAGATCAACGA 408
DB 97 LeuthrPheGlyGlyGlyThrIysValGluIleIysArg 109

RESULT 7
KV3L_HUMAN
ID KV3L_HUMAN STANDARD; PRT; 129 AA.
AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region HAH precursor.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=68171307; PubMed=3127527;
RA Kippes T.J., Tomhave R., Chen P.P., Carson D.A.;
RT "Antibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -I- DISASE: The protein is one of the surface immunoglobulin M
CC autointibodies expressed in patients with chronic lymphocytic
CC leukemia.
DR PIR; P10022; K3H0HA.
DR HSSP; P01625; 1EQ.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; P:immune response; NAS.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 1 129 Ig kappa chain V-III region HAH.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 55 Complementarity-determining-1.
FT DOMAIN 56 70 Framework-2.
FT DOMAIN 71 77 Complementarity-determining-2.
FT DOMAIN 78 109 Framework-3.
FT DOMAIN 110 118 Complementarity-determining-3.
FT DOMAIN 119 129 Jkl segment.
FT DISULFID 43 109 By similarity.
FT NON_TER 129
SQ SEQUENCE 129 AA; 14073 MW; D3C5529277274D0 CRC64;

Alignment Scores:
Pred. No.: 9.97e-32 Length: 129
Score: 526.00 Matches: 103
Percent Similarity: 95.58% Conservative: 5
Best Local Similarity: 91.15% Mismatches: 1
Query Match: 30.71% Indels: 4
DB: 1 Gaps: 1

US-09-194-164-13 (1-918) x KV3L_HUMAN (1-129)
QY 70 GATATTGTTGACGAGCTCCAGGACCTGTTGCTCCAGGGGAAAGAGCCACC 129
DB 21 GuileValIeuthrGlnSerProGlyThrLeuSerLeuSerProGlyGluIleValThr 40
QY 130 CTCTCTGAGGGCCAGTGCAGAGTGTAGTACGACTTACCTGGTACGACGAGAA 189
DB 41 LeuSerCysArgIleSerGlnSerValSerSerSerTyrIleuIleAlaTyrTyrGlnGlnIys 60

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QY 190 CTGGCCAGGCTCCAGGCTCTCTATCTATGTGATCCACAGGGCCACTGGCATGCCA 249
DB 61 ProgiGlnAlaIleProIArgLeuIleTyrTyrGlyAlaSerSerArgAlaThrIleIlePro 80
QY 250 GACAGATTTCAGTGCAGAGTGGGTCGGGACAGACTTCATCTCACCATAGTAGTGGAG 309
DB 81 AsparGlnSerGlySerGlySerGlyThrAspPheThrIleSerArgLeuGln 100
QY 310 CCTGAAGATTTCAGGTGATTACTGTGCAGAGTATGTAGTCACTCAGACACCTCAG 369
DB 101 ProgiuaApPheAlaValTyrTyrCysGlnGlnTyrGlyThrSerProArg----- 117
QY 370 ATCACTTTGGCGGAGGAGCCAGAGTGGAGATCAACGA 408
DB 118 ---ThrPheGlyGlnGlyThrIysValGluIleIysArg 129

RESULT 8
KV3B_HUMAN
ID KV3B_HUMAN STANDARD; PRT; 109 AA.
AC P01620;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE IG kappa chain V-III region SIE.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
[1]
RP SEQUENCE.
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human IgM anti-gamma-globulins of the wa
RT group.";
RL Biochemistry 20:5816-5822(1981).
CC -I- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC globulin activity.
DR PIR; A01892; K3H0SI.
DR HSSP; P01625; 1LVE.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; P:immune response; NAS.
DR Direct protein sequencing; Immunoglobulin V region.
FT DISULFID 23 89 By similarity.
FT NON_TER 109
SQ SEQUENCE 109 AA; 11775 MW; 76899C3BCD646FFB4 CRC64;

Alignment Scores:
Pred. No.: 1.65e-31 Length: 109
Score: 523.00 Matches: 102
Percent Similarity: 95.58% Conservative: 6
Best Local Similarity: 90.27% Mismatches: 1
Query Match: 30.53% Indels: 4
DB: 1 Gaps: 1

US-09-194-164-13 (1-918) x KV3B_HUMAN (1-109)
QY 70 GATATTGTTGACGAGCTCCAGGACCTGTTGCTCCAGGGGAAAGAGCCACC 129
DB 1 GuileValIeuthrGlnSerProGlyThrLeuSerLeuSerProGlyGluIleValThr 20
QY 130 CTCTCTGAGGGCCAGTGCAGAGTGTAGTACGACTTACCTGGTACGACGAGAA 189
DB 21 LeuSerCysArgIleSerGlnSerValSerSerSerTyrIleuIleAlaTyrTyrGlnGlnIys 40
QY 190 CTGGCCAGGCTCCAGGCTCTCTATCTATGTGATCCACAGGGCCACTGGCATGCCA 249

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Db      41 ProGlyGlnAlaProArgLeuLeuIleTyrGlyAlaSerSerArgAlaThrGlyIlePro 60
Oy      250 GACAGCTTCAGTGGAGAGTGGGTCCGGGACAGACTTCACCTCAGATCAGTGGAG 309
Db      61 AsparGpneSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerTrgLeuGln 80
Oy      310 CCTGAAGATTTCAGATGATTACTGTGCAGAGTATGGTAGCTCAGCTCAGACCTCAG 369
Db      81 ProAspAspPheAlaValIleTyrTyrCysGlnGlnIleTyrGlySerSerProGln----- 97
Oy      370 ATCACTTTCCGGCGAGGAGGACCAAGGTGGAGATCAACCA 408
Db      98 ---ThrpheGlyGlnGlySerIleValGlnIleLysArg 109

```

## RESULT 9

KV3M\_HUMAN  
ID KV3M\_HUMAN STANDARD; PRT; 129 AA.

AC P18136;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-II region HIC precursor.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI\_TaxId=9606;

RA MEDLINE=88171307; PubMed=3127527;

RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;

RT "Autoantibody-associated kappa light chain variable region gene

RT expressed in chronic lymphocytic leukemia with little or no somatic

RT mutation. Implications for etiology and immunotherapy.";

RL J. Exp. Med. 167:840-852(1988).

-I- DISEASE: The protein is one of the surface immunoglobulin M

autocantibodies expressed in patients with chronic lymphocytic

leukemia.

CC PIR; P10021; K3H0H1.

DR HSP; P01625; 1EB0.

DR GO; GO:0005576; Cxcracellular; NAS.

DR GO; GO:0003823; P:antigen binding; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig\_V.

DR Pfam; PF00047; Ig\_V.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG\_LIKE; 1.

KW Immunoglobulin V region; Signal.

FT SIGNAL 1 20

FT CHAIN 21 129 Ig kappa chain V-II region HIC.

FT DOMAIN 21 43 Framework-1.

FT DOMAIN 44 55 Complementarity-determining-1.

FT DOMAIN 56 70 Framework-2.

FT DOMAIN 71 77 Complementarity-determining-2.

FT DOMAIN 78 109 Framework-3.

FT DOMAIN 110 118 Complementarity-determining-3.

FT DOMAIN 119 129 Jkl segment.

FT DISULFID 43 109 By similarity.

FT NON\_TER 129 129

SO SEQUENCE 129 AA; 14070 MW; 7395528EA2B74D6 CRC64;

## Alignment Scores:

Pred. No.: 2,86e-31 Length: 129  
Score: 520.00 Matches: 103  
Best Local Similarity: 93.81% Conservative: 3  
Best Local Similarity: 91.15% Mismatches: 3  
Query Match: 30.36% Indels: 4  
Gaps: 1

US-09-194-164-13 (1-918) x KV3M\_HUMAN (1-129)

Oy 70 GATATTGTTGACGACGAGTCTCCAGGACCCCTGTTCTTTCTTCACGGGAAAGCCACC 129

```

Db      21 GlnIleValLeuThrGlnSerProGlyThrLeuSerLeuSerProGlyGlnTrgAlaThr 40
Oy      130 CTCCTCTCAGGAGGACGAGTTCAGAGTGTAGTACAGCTTACTTACCTGATACAGGAA 189
Db      41 LeuSerCyArGAlaIleSerGlnSerValSerSerTrpLeuAlaIleTrpGlnGln 60
Oy      190 CTGGCCAGGCTCCAGGCTCCTCATCTATAGTGCATCCAGGACCAAGGACCACTGCA 249
Db      61 ProGlyGlnAlaProArgLeuLeuIleTyrGlyAlaSerSerArgAlaThrGlyIlePro 80
Oy      250 GACAGCTTCAGTGGAGAGTGGGTCCGGGACAGACTTCACCTCAGATCAGTGGAG 309
Db      81 AsparGpneSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerTrgLeuGln 100
Oy      310 CCTGAAGATTTCAGATGATTACTGTGCAGAGTATGGTAGCTCAGCTCAGACCTCAG 369
Db      101 Pro***AspPheAlaValIleTyrTyrCysGlnGlnIleTyrGlySerSerProTrp----- 117
Oy      370 ATCACTTTCCGGCGAGGAGGACCAAGGTGGAGATCAACCA 408
Db      118 ---ThrpheGlyGlnGlySerIleValGlnIleLysArg 129

```

## RESULT 10

Q8WUK1  
ID Q8WUK1 PRELIMINARY; PRT; 613 AA.

AC Q8WUK1;

DT 01-MAR-2002 (TREMBLrel. 20, Created)

DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)

DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE IGHM protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI\_TaxId=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Primary B-Cells;

RX MEDLINE=22388257; PubMed=1477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stabileton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultx S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Primary B-Cells;

RA Strausberg R.L.

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC020240; AAH20240.1; --

DR PIR; P36005; P36005.

DR PIR; G36005; G36005.

DR PIR; PH1642; PH1642.

DR PIR; PH1643; PH1643.

DR PIR; PH1645; PH1645.

DR PIR; PH1646; PH1646.

DR PIR; P10098; P10098.

DR PIR; P10120; P10120.







DR GO:0005576; C:extracellular; NAS.  
 DR GO:0003823; F:antigen binding; NAS.  
 DR GO:0006955; F:immune response; NAS.  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003596; IG\_v.  
 DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00406; IGV: 1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 DR Direct protein sequencing; Immunoglobulin V region.  
 FT DISULFID 23 By similarity.  
 FT NON TER 109  
 SQ SEQUENCE 109 AA; 11746 MW; 566C15B6B9CBE6 CRC64;

Alignment Scores:  
 Pred. No.: 3.27e-30 Length: 109  
 Score: 506.00 Matches: 100  
 Percent Similarity: 92.04% Conservative: 4  
 Best Local Similarity: 88.50% Mismatches: 5  
 Query Match: 29.54% Indels: 4  
 DB: 1 Gaps: 1

US-09-194-164-13 (1-918) x KV3E\_HUMAN (1-109)

QY 70 GATATTGTTGACGAGCTCTCCAGGACCCCTGTTGTCCTCAGGGGAAAGCCACC 129  
 Db 1 GlnIleValLeuThrGlnSerProGlyThrLeuSerLeuSerProGlyGlnArgAlaThr 20

QY 120 CTCTCTCAGAGGCGCAGTCAAGTGTAGTACAGCTACTTACCTGTGATCCAGAGAA 189  
 Db 21 LeuSerCybArgAlaSerGlnSerValSerSerGlyTyrLeuGlyTyrPyrGlnGln 40

QY 190 CTGGCCAGGCTCCAGGCTCTCTCATCTATGGTGATCCACAGGCGCCATGGCATGCCA 249  
 Db 41 ProGlyGlnAlaProArgLeuLeuLeuTyrGlyAlaSerSerArgAlaThrGlyLeuPro 60

QY 250 GACAGTTTCAGTGGAGGAGTGGCTCCGAGACAGACTTCACCTCAGCATGATGAGGAG 309  
 Db 61 AsparGlnSerSerGlySerGlySerGlyThrAspPheThrIleSerArgLeuGln 80

QY 310 CCTGAAGATTTCAGTGTATTACTGTCTGACAGATAGTGTAGTCACTTCAGACACCTCAG 369  
 Db 81 ProGlnAspPheAlaValTyrTyrCysGlnGlnTyrGlySerLeuGlyArg----- 97

QY 370 ATCACTTTCCGCGGAGGAGCCAGGTGAGATCAACGA 408  
 Db 98 ---ThrPheGlyGlnGlyThrIleValGlnIleLeuArg 109

RESULT 13

Q65ZC9 PRELIMINARY; PRT; 240 AA.  
 AC Q65ZC9;  
 DT 25-OCT-2004 (TREMBLrel. 28, Created)  
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)  
 DE Single-chain Fv (Fragment).  
 GN Name=bcFv;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C14/7;  
 RX MEDLINE=97362799; PubMed=9219263;  
 RA Kontermann R.E., Wing M.G., Winter G.;  
 RT "Complement recruitment using bispecific diabodies";  
 RL Nat. Biotechnol. 15:629-631(1997).  
 DR EMBL; Y13056; CAA73499.1; -.  
 DR InterPro: IPR003599; IG.  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003596; IG\_v.  
 DR Pfam: PF00047; Ig\_2.  
 DR SMART; SM00409; IG; 2.

DR SMART; SM00406; IGV: 2.  
 DR PROSITE; PS50835; IG\_LIKE; 2.  
 FT NON TER 1  
 FT NON TER 240  
 SQ SEQUENCE 240 AA; 25569 MW; FDCFD3645F64B373 CRC64;

Alignment Scores:  
 Pred. No.: 3.66e-30 Length: 240  
 Score: 506.00 Matches: 101  
 Percent Similarity: 84.13% Conservative: 5  
 Best Local Similarity: 80.16% Mismatches: 12  
 Query Match: 29.54% Indels: 8  
 DB: 2 Gaps: 2

US-09-194-164-13 (1-918) x Q65ZC9 (1-240)

QY 478 CAGGTGACGCTGTGATGATGCTGGGAGGCGGTGTCAGGCTGGAGGTCCTGAGACTC 537  
 Db 1 GlnValGlnLeuValGlnSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20

QY 538 TCCTGTGACGCTGTGATTCCTCCCTTCAGAACCTTGTCTATGCACTGGTCCGACGCT 597  
 Db 21 SerCysAlaAlaSerGlyPheThrPheSerSerTyrGlyMetIleTyrValArgGlnAla 40

QY 538 CTAGGCAAGGCGCTGAGTGGGTGGCACTTATATCATATGATGAGACACTAAATATAC 657  
 Db 41 ProGlyLeuGlyLeuGlnTyrValAlaValIleSerTyrAspGlySerAsnIleTyr 60

QY 658 GCAGACTCCGAGAGGCGGATTCACATCTCCAGAGACACTTCCAGAACAGGCTGTAT 717  
 Db 61 AlaAspSerValGlyGlyArgPheThrIleSerArgAspAsnSerLeuAsnThrLeuTyr 80

QY 718 CTAAATAATGACAGCTTGAAGACTGAGAGACAGCGCTGTCTATTACTGTGCGAGATCAG 777  
 Db 81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyrTyrCysAlaIleArgAsp 99

QY 778 AGCTGTGGGTGATATGACACACTACGCTTGGACAGTGTGGGCGAAAGGACGACG 837  
 Db 100 -----TyrGlyAsp-----SerLeuAspProTyrGlyLeuThrLeu 112

QY 838 GTCACTGCTCCTCAGGA 855  
 Db 113 ValThrValSerSerGly 118

RESULT 14

HV3G\_HUMAN STANDARD; PRT; 122 AA.  
 ID HV3G\_HUMAN  
 AC P01768;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Ig heavy chain V-III region CAM.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=81013859; PubMed=6774332;  
 RA Lehman D.W., Putnam F.W.;  
 RT "Amino acid sequence of the variable region of a human mu chain:  
 location of a possible JH segment";  
 RL Proc. Natl. Acad. Sci. U.S.A. 77:3235-3243(1980).  
 CC -1- MISCELLANEOUS: This mu chain was isolated from the plasma of a  
 CC patient with macroglobulinemia.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A02051; M3HRAM.  
 DR HSSP; P01772; 2FB4.  
 DR GO:0005576; C:extracellular; NAS.  
 DR GO:0003823; F:antigen binding; NAS.  
 DR GO:0006955; F:immune response; NAS.  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003596; IG\_v.

DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR Direct protein sequencing; Immunoglobulin V region;  
 KW Pyrolydione carboxylic acid.  
 FT DOMAIN 1 112 Ig-like.  
 FT MOD RES 1 1 Pyrolydione carboxylic acid.  
 FT NON\_TER 122 122  
 SQ SEQUENCE 122 AA; 13666 MW; A42D0F17D252F1C2 CRC64;

Alignment Scores:  
 Pred. No.: 1,24e-29 Length: 122  
 Score: 498.50 Matches: 93  
 Percent Similarity: 86.40% Conservative: 15  
 Best Local Similarity: 74.40% Mismatches: 14  
 Query Match: 29.10% Indels: 3  
 DB: 1 Gaps: 1

US-09-194-164-13 (1-918) x HV3G\_HUMAN (1-122)

QY 478 CAGGTGACGCTGCTGAGTCTCTGGGGAGCGCTGCTCAGCTGGAGGTCTCTGAGACTC 537  
 |||:::|||||  
 DB 1 GIUVALGLEUVALGILSERGLYGLYVAL\*\*PROGLYARGSERLEUARGLEU 20  
 |||:::|||||

QY 538 TCCTGTCAGCTCTGATTCCTCCCTCAGAGCTTGATGACCTGCGCGCAGGCT 597  
 |||:::|||||  
 DB 21 SERCYBALAALASERGLYPHERTHRPHESERASRYALAMECHISTRIPALARGINPRO 40  
 |||:::|||||

QY 598 CTAGGCAAGGGCTGAGTGGGTGGGAGCTTATATCATATGATGAGACCAATAACTAC 657  
 |||:::|||||  
 DB 41 PROGLYLYGLYLENGILTRIPALALVALLESERTY\*\*GLY\*\*\*\*\*LYSTYTRYR 60  
 |||:::|||||

QY 658 GAGAGCTCCGTGAAGGCCGATTCACCATCTCCAGAGACACTTCCAAAGACCGTGAT 717  
 |||:::|||||  
 DB 61 AIA\*\*SERVALLYGLYARGPHERTHRILLESERARGASP\*\*SERLYS\*\*THRILEUTYR 80  
 |||:::|||||

QY 718 CTAAATAATGACAGCTGAGAACTGAGACAGCGGCTGTATATTACTGTGCGAGATCG 777  
 |||:::|||||  
 DB 81 LEUGIMETASERLEUARGALAGLU\*\*THRALVALTYRTRYCYBALARGSPARG 100  
 |||:::|||||

QY 778 AGCCTGTGGGTGACTATGACCACTACGAGTGTGAGCGTGGGCAAGGAGCAAG 837  
 |||:::|||||  
 DB 101 PROLEUTYRGLY\*\*TYRARGALAPHE\*\*\*\*\*ASNTYTRIPGLYGLNGLYTHRIEN 117  
 |||:::|||||

QY 838 GTACCCGTCTCTCA 852  
 |||:::|||||  
 DB 118 VALTHRVALSERSER 122  
 |||:::|||||

RESULT 15  
 Q9UL86 PRELIMINARY; PRT; 109 AA.

AC Q9UL86, 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Myosin-reactive immunoglobulin kappa chain variable region (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cclin.1998.4531;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL; AF035028; AAD56264.1; -.  
 DR PIR; I30601; I30601.  
 DR HSP; P01625; IERK3.

DR InterPro; IPR007110; Ig-like.  
 DR SMART; SM003596; IG\_LV.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR NON\_TER 109 109  
 FT NON\_TER 109 109  
 SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DACC83 CRC64;

Alignment Scores:  
 Pred. No.: 1.59e-29 Length: 109  
 Score: 497.00 Matches: 99  
 Percent Similarity: 91.15% Conservative: 4  
 Best Local Similarity: 87.61% Mismatches: 6  
 Query Match: 29.01% Indels: 4  
 DB: 2 Gaps: 1

US-09-194-164-13 (1-918) x Q9UL86 (1-109)

QY 70 GATATGTTGAGCGCACTCTCCAGGACCCCTGCTTGTCTCCAGGGGAAAGACCAAC 129  
 |||:::|||||  
 DB 1 GIUVALGLEUVALGILSERPROGLYTHRLEUSERLEUPHEPROGLYGLNARGALATHR 20  
 |||:::|||||

QY 130 CTCTCTGCAAGGCCAGTCAAGATGTTAGTACAGCTACTTAGCTGTGATCCAGCAAGAA 189  
 |||:::|||||  
 DB 21 LEUSERCYBALASERGLINSEVALSERISERTYRLEUALATRTYGLINGLNYS 40  
 |||:::|||||

QY 190 CTTGGCCAGGCTCCAGGCTCTCATCTATGTGTCATCCACGAGGCCACTGGCATGCCA 249  
 |||:::|||||  
 DB 41 PROGLYGLNALAPROARGLEUULETYRGLYTHRISERARGALATHRGLYLEPRO 60  
 |||:::|||||

QY 250 GACAGGTCAGTGGAGGAGGAGGAGCGGAGCACTTCACTTCACATGATAGATGAGG 309  
 |||:::|||||  
 DB 61 ASPARGPHESEGLYSERGLYSERGLUTHRASPHEMTRLEUTHILLESERARGLEUDU 80  
 |||:::|||||

QY 310 CTTGAAGATTTTGAGTGTATTACTGTGACAGAGTATGTAGTCACTCCAGACACTCAG 369  
 |||:::|||||  
 DB 81 PROGLUASPHEALVALTYRTRYCYSEGLNGLNTRYGLYSERSE\*\*\*\*\*ILE 96  
 |||:::|||||

QY 370 ATCACTTTGGCGGAGGAGCAAGGTGAGATCAACGA 408  
 |||:::|||||  
 DB 97 PHETHRPHGLYPROGLYTHRILYSVALASPILLEYSARG 109  
 |||:::|||||

Search completed: February 18, 2005, 08:45:55  
 UOB time : 114 secs

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: February 18, 2005, 06:09:18 ; Search time 94.5 Seconds  
(without alignments)  
7514.202 Million cell updates/sec

Title: US-09-194-164-13  
Perfect score: 1713  
Sequence: 1 GAATTCATGAAAAAACCCG.....ATCACATTAGTAAGCTT 918

Scoring table:  
BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODE=frame+12p\_model -DEV=xlh  
-O=/cgn2\_1/USPRO.epool/US09194164/runat\_16022005\_122612\_6012/app\_query.fasta\_1.1095  
-DB=4 Geneseq\_16Dec04 -QEMT=faeacan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsu62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTPRT=pct -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09194164 @CGN\_1\_1101 @runat\_16022005\_122612\_6012 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6  
-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -Delop=6 -Delext=7

Database :  
1: Geneseq\_16Dec04:\*  
2: geneseqp1980s:\*  
3: geneseqp1990s:\*  
4: geneseqp2000s:\*  
5: geneseqp2001s:\*  
6: geneseqp2002s:\*  
7: geneseqp2003as:\*  
8: geneseqp2003bs:\*  
9: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1573	91.8	304	2	AAW40070 Human H11
2	1573	91.8	304	2	AAE00947 Human mon
3	1573	91.8	304	7	ABU10486 C-antigen
4	1573	91.8	304	8	ADOS2296 Human ant
5	1451.5	84.7	287	2	AAW40071 Human H11
6	1451.5	84.7	287	4	AAE00948 Human mon
7	1451.5	84.7	287	7	ABU10487 C-antigen
8	1451.5	84.7	287	8	ADOS2299 Human ant
9	1016.5	59.3	638	6	ADA89103 Phage dis
10	1016.5	59.3	638	6	ADA90139 Anti-Abet

11	1016.5	59.3	638	6	ADA91410 Anti-Abet
12	1016.5	59.3	747	7	ADG74355 MSPRO 11g
13	986	57.6	523	3	AAV44994 HD708CFV-
14	986	57.6	524	3	AAV44995 HD708CFV-
15	972.5	56.8	628	6	ABJ38670 Fab expre
16	961.5	56.1	252	8	ADOS8062 S2 cell d
17	928	54.2	352	2	AAV06272 Anti-Fc g
18	916.5	53.5	295	5	ABG68848 C219cFV
19	914	53.4	490	3	AAV56637 hCATL Bln
20	892	52.1	283	5	AAU75160 Kabat con
21	892	52.1	283	5	ABG73148 Kabat con
22	892	52.1	283	5	ABG73868 Kabat con
23	891.5	52.0	319	5	ABG68851 Interfero
24	887	51.8	263	2	AAW97889 Kabat con
25	866.5	50.6	630	7	ADG69023 Chloropia
26	866.5	50.6	639	7	ADG68991 Chloropia
27	865	50.5	354	3	AAV82515 Anti-HA P
28	863.5	50.4	277	7	ADG69018 Human chl
29	858.5	50.1	250	8	AD161980 Human bcf
30	857.5	50.1	279	7	ABR61568 HIV-1 neu
31	849.5	49.6	252	8	ADG40405 Single ch
32	849.5	49.6	252	8	ADG40409 Single ch
33	849.5	49.6	253	8	ADG40406 Single ch
34	849.5	49.6	254	8	ADG40412 Single ch
35	847	49.4	239	8	ADG40413 Single ch
36	846.5	49.4	484	6	ABR55341 Amino act
37	840	49.0	247	7	ADG03132 Colon spe
38	834.5	48.7	254	8	ADG17470 HIV envel
39	828.5	48.4	487	6	ADG17475 HIV envel
40	828	48.3	650	6	ABR62591 Anti-CD7
41	828	48.3	651	6	ABR62590 Anti-CD7
42	824.5	48.1	247	8	ADG40408 Single ch
43	824.5	48.1	254	8	ADG17468 HIV envel
44	824	48.1	443	6	ABG76488 Humanised
45	824	48.1	443	6	ABG74240 Chimæric

## ALIGNMENTS

RESULT 1	AAW40070 standard; protein; 304 AA.
ID	AAW40070
AC	AAW40070;
XX	
DT	29-MAY-1998 (first entry)
XX	
DE	Human H11-scFv construct monomer forming protein.
XX	
KW	H11; monoclonal antibody; Mab; C-antigen; variable region heavy chain;
KW	V region; H chain; neoplasia; detection; lymphoma; tumour cell; probe;
KW	primer; vaccine; gene therapy; glioblastoma; neuroblastoma;
KW	malignant melanoma; adenocarcinoma; small cell lung carcinoma;
KW	single chain variable region; scFv.
OS	Synthetic.
OS	Homo sapiens.
XX	
PN	W09744461-A2.
XX	
PD	27-NOV-1997.
XX	
PF	22-MAY-1997; 97WO-US008962.
XX	
PR	22-MAY-1996; 96US-00657449.
XX	
PA	(NOVO-) NOVOPHARM BIOTECH INC.
XX	
PI	Dan MD, Matci FK, Kaplan HA;
XX	
DR	WPI; 1998-018515/02.
XX	
DR	N-PSDB; AAV10118.
XX	

PT Antigen binding fragment from monoclonal antibody, H11 - allows tumour  
 specific detection and treatment of neoplasia.

XX Claim 5; Page 92-93; 126bp; English.

XX This sequence represents a human H11 monoclonal antibody single chain V  
 CC region fragment (H11-scFv) construct which is capable of forming  
 CC monomers. This construct is used to determine the ability of H11-scFv  
 CC antibody fragments to bind specifically to the C-antigen on cancer cells.  
 CC Such antigen binding fragments may be used for treating a patient with  
 CC neoplasia. It is especially useful in the detection of lymphomas and  
 CC leukaemias where the tumour cells bearing the C antigen are circulating  
 CC in the patients bloodstream. The polynucleotide sequence may be used as a  
 CC primer or a probe and the encoded protein may be used in a vaccine or for  
 CC gene therapy. The human monoclonal antibody (Mab), designated H11,  
 CC specifically recognises cancerous cells. H11 is specific for  
 CC glioblastoma, neuroblastoma, malignant melanoma, breast adenocarcinoma,  
 CC lung adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and  
 CC prostate adenocarcinoma

XX Sequence 304 AA;

Alignment Scores:

Pred. No.:	3.9e-118	Length:	304
Score:	1573.00	Matches:	302
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	91.83%	Indels:	0
DB:	2	Gaps:	0

US-09-194-164-13 (1-918) x AAM40070 (1-304)

QY	1	GAATTCATGAAAAAAACCGCTATCGCGATGCGATGTCAGTGGCTGTTGGCTACCGTT	60
DB	1	GIuphemelLylyshrrAlaIleAlaIleAlaValAlaIleAlaGlyPheAlaThrVal	20
QY	61	GGCGAGGCGGATATTTGTTGACGCGATCTCCAGGACCCCTGTTGTTCTCCAGGGGAA	120
DB	21	AlaGlnAlaAspIleValleuThrGlnSerProGlyThrLeuSerLeuSerProGlyGln	40
QY	121	AAGACGACCTCTCCGCGAGGCGCGATGCGATGAGTGTAGTACGACTTACGCTGTAC	180
DB	41	ArgAlaThrLeuSerCysArgAlaSerGlnSerValSerSerSerYrleuAlaTrpYr	60
QY	181	CAGCAGAAACCTGGCCAGGCTCCAGGCTCTCATGATGATGATGATCCACGAGGCACT	240
DB	61	GlnGlnLyProGlyGlnAlaProArgLeuLeuIleTyrGlyAlaSerThrArgAlaThr	80
QY	241	GGCATGCCAGACGATGTCAGTGGCTCCGGACAGACTTCACTTCCATCAGT	300
DB	81	GlyMetProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSer	100
QY	301	AAGATGGAGCCTGGAATTTTTCAGTGTATTAATGTCAGAGATGATGATGATGATGAT	360
DB	101	ArgLeuGlnProGlnAspPheAlaValIYrTyrCysGlnGlnIYrTyrLeuSerSerProGln	120
QY	361	ACAACCTCAGATCACTTTCGCGAGGAGCCAGGATGAGTGAATCAACGAACTGTGCTGA	420
DB	121	ThrProGlnIleThrPheGlyGlyGlyThrIleValIleGlnIleYsrArgThrValAlaIa	140
QY	421	CCATCTGTCTTGGCGGCTGGCGGTTCCGAGGTGTGTGATCAGTGTGAAGTGGCTCCG	480
DB	141	ProSerValSerIYrGlyGlySerGlyGlyGlySerIYrGlyGlySerGlyGlySerGln	160
QY	481	GTGACAGCTGGTGGAGCTGGGAGGAGGTGTGTCAGGCTGGAGGATCCCTGAGACTCC	540
DB	161	ValGlnIleuValGlnSerGlyGlyValValGlnProGlyArgSerLeuAlaGlnSer	180
QY	541	TGTGACGCTCTGATTTCCCTTCAAGAGCTTTGCTATGATGATGATGATGATGATGAT	600
DB	181	CysAlaIaIaSerClyPheProPheArgSerPheAlaMetHisTrpValArgGlnAlaIe	200
QY	601	GGCAAGGGCTGAGTGGGTGGGCAATTATATCATATGATGAGCAACTAAATCTACGCA	660

DB	201	GIlyySGlyLeuGIuTrpValAlaValIleSerTyrAspGlySerThrIySerTyrTrAla	220
QY	661	GACTCCGTGAAGGGCCGATTCACATCTCCAGACACTTCCAGAACACGCTGATCTTA	720
DB	221	AspSerValIySGlyArgPheThrIleSerArgPheTrnSerIyAsnThrValIyTrleu	240
QY	721	AAATGAACAGCCTGAGAACCTGAGACACGCGCTGCTTTCGTGCGAGATGACAGGC	780
DB	241	LySMeTasnSerLeuArgThrGlnAspThrAlaValIYrTyrCysAlaArgAspGlnSer	260
QY	781	CTGTGGGTGACTATGACCACTACTACGTTTGGACGTCTGGGCGCAAGGACACGCTC	840
DB	261	LeuLeuGlyAspTyrAspHisTyrTyrGlyLeuAspValITrpGlyLySGlyThrThrVal	280
QY	841	ACCGTCTCTCAGATTCGGAACAAACTGATGACGCAAGAAATCTGATCACTACCAT	900
DB	281	ThrValSerSerGlySerGlnGlnLySLeuIleSerGlnGluAspLeuAsnHisHis	300
QY	901	CACCAT 906	
DB	301	HisHis 302	

RESULT 2  
 AAE00947 standard; protein; 304 AA.  
 ID AAE00947  
 AC AAE00947;  
 XX  
 XX  
 DT 04-JUL-2001 (first entry)

Human monoclonal antibody H11-single chain variable region (scfv) #1.

Human; monoclonal antibody; Mab; H11; single chain variable region; scfv;  
 KW neoplastic disease; melanoma; immunoglobulin IgM; gene therapy; lymphoma;  
 KW carcinoma; breast; lung; gastric; prostate; ovary; colon; lung; vaccine;  
 KW neuroblastoma; soft tissue sarcoma; prostatic adenocarcinoma; cytostatic;  
 KW C-antigen; chronic leukemia; glioma.

OS Homo sapiens.

XX	Key	Location/Qualifiers
FX	Region	144..158
FT		/label= Linker
FT	Misc-difference	302..303
FT		/note="Encoded by CATTAGTGAAG"

US6207153-B1.

27-MAR-2001.

22-MAY-1997; 97US-00862124.

22-MAY-1996; 96US-00657449.

(VIVE-) VIVENTIA BIOTECH INC.

Dan MD, Maici PK, Kaplan HA;

WPI; 2001-289584/30.

N-PSDB; AAD04537.

Composition comprising antigen binding fragments of an antibody that  
 PT recognizes an antigen on neoplastic cells but not on normal cells for use  
 PT in diagnosis, imaging and treatment of carcinomas.

Claim 1; Col 63-66; 56bp; English.

The present sequence is human monoclonal antibody (Mab), H11-single chain  
 CC variable region (scfv). The H11 light chain variable region is linked to  
 CC the heavy chain variable region through a (SGGGG)3 linker to form  
 CC monomers. The invention relates to human monoclonal antibody (Mab) H11,  
 CC H11-(scfv) single chain variable (V) region fragment and their

CC corresponding DNA molecules. H11 antibody is an immunoglobulin of IgM  
 CC subunits which is specific to C-antigen found specifically on neoplastic  
 CC cells and not on normal cells. H11 is an antibody obtained from the  
 CC fusion of peripheral blood lymphocytes of a 64 year old male with a low  
 CC grade glioma and fused to a human myeloma cell line to produce a  
 CC hybridoma designated NBGM1/H11. A pharmaceutical composition comprising  
 CC H11 and its derivatives are useful in the diagnosis, imaging and  
 CC treatment of neoplastic disease, particularly, melanoma, breast  
 CC carcinoma, lung carcinoma, ovarian carcinoma, colon carcinoma, gastric  
 CC carcinoma, prostate carcinoma, lymphoma carcinoma, neuroblastoma, glioma,  
 CC soft tissue sarcoma, small cell lung carcinoma, prostatic adenocarcinoma,  
 CC B and T cell lymphomas and chronic leukemias. H11 DNA is also used in  
 CC vaccines and gene therapy

xx Sequence 304 AA:

Alignment Scores:  
 Pred. No.: 3,9e-118 Length: 304  
 Score: 1573.00 Matches: 302  
 Percent Similarity: 100.00% Conservatave: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 91.83% Indels: 0  
 DB: 4 Gaps: 0

US-09-194-164-13 (1-918) x AAB00947 (1-304)

QY 1 GAATTCATGAAAAAACCCTATCGCGATGCGAGTTGCACTGGCTGGTTGGCTACCGTT 60  
 Db 1 GIUPMECTLYLGTThrAlaIleAlaIleAlaValAlaLeuAlaGlyPheAlaThrVal 20  
 QY 61 GCGGAGCGCGATATTGTGTGACGAGCTCCAGGACCCCTCTTTGGTCCAGGGAA 120  
 Db 21 AlaGlnAlaAspIleValLeuThrGlnSerProGlyThrLeuSerLeuSerProGlyGlu 40  
 QY 121 AGAGCCACCTCTCTCGAGAGGCGCAGTCAAGTGTAGTACGAGTCACTTACCTGTATC 180  
 Db 41 ArgAlaThrLeuSerCysArgAlaSerGlnSerValSerSerSerTyrLeuAlaTrpTyr 60  
 QY 181 CAGCAGAAACCTGGCGCAGGCTCCAGGCTCTCATCTATGTATGTGATCCACGAGGCCACT 240  
 Db 61 GlnGlnIlybProGlyGlnAlaProArgLeuLeuIleTyrGlyAlaSerThrArgAlaThr 80  
 QY 241 GGCATGCCAGACAGGTTGAGTGGAGTGGGTCGGGAGACAGATTGACTCTACCATCACT 300  
 Db 81 GlyMetProAspArgPheSerIleSerIleSerGlyThrAspPheThrLeuThrIleSer 100  
 QY 301 AGACTGAGCCTGAGATTTTGTGCACTGTATTAAGTGTGAGTATGATGATGATGATGAT 360  
 Db 101 ArgLeuGluProGluAspPheAlaValTyrTyrCysGlnGlnIlybIleSerProGln 120  
 QY 361 ACACCTCAGATCACTTTGGCGGAGGAGCAAGGTGAGATCAAGCAAGTGTGGCTGCA 420  
 Db 121 ThrProGlnIleThrPheGlyGlyIlybIlybValGlnIleIlybAlaArgThrValAla 140  
 QY 421 CCATCTGTCTCTGGGCGTGGCGGTCCTCCGAGGTGTGATCAGTGTGAGTGGTCTCCAG 480  
 Db 141 ProSerValSerGlyGlyIlybIlybIlybIlybIlybIlybIlybIlybIlybIlyb 160  
 QY 481 GTGAGCTGTGAGTGTGGGAGGCGTGTGCGAGCTGGGAGGCTCCCTGAGATCTCC 540  
 Db 161 ValGlnLeuValGlnSerGlyGlyIlybIlybValGlnProGlyArgSerLeuArgLeuSer 180  
 QY 541 TGTGAGCCTCTGATTCCTCTCAGAGCTTTGTATGCACTGGGTCGGCGAGCTCTA 600  
 Db 181 CysAlaAlaSerGlyPheProPheArgSerPheAlaMetIleTrpValArgGlnAlaLeu 200  
 QY 601 GGCAGAGGCGTGGAGTGGGAGTGTATATCATATGATGAGAGCACTAAATACATCAACA 660  
 Db 201 GlyIlybGlyLeuGluTrpValAlaValIleSerTyrAspGlySerThrIlybTyrTyrAla 220  
 QY 661 GACTCCGTGAAGGCGCATTCATCTCCAGAGACACTTCCAGAGACAGGATGATCTA 720  
 Db 221 AspSerValIlybGlyArgPheThrIleSerArgAspThrIleSerIlybAlaThrValTyrLeu 240

QY 721 AAAATGACAGCCTGAGAACTGAGACACAGGCTGTCTATTACTTCCGAGATCAAGAC 780  
 Db 241 IySweIaSerLeuArgThrGluAspThrAlaValTyrCysAlaArgAspGlnSer 260  
 QY 781 CGTTGGGTGATATGACCACTACTACGTTTGAAGTGTGGGCAAGGACACAGGTC 840  
 Db 261 LeuLeuGlyAspTyrAspThrIlybIlybValIlybGlyValIlybThrVal 280  
 QY 841 ACCGTCCTCAGATTCGAGCAAAAGTATCAGCGAAGAGATCTGAACCATCAACAT 900  
 Db 281 ThrValSerSerGlySerGlnIlybIlybLeuIleSerGluGluAspLeuAsnIleHis 300  
 QY 901 CACCAT 906  
 Db 301 HSHIS 302

RESULT 3  
 ABU10486  
 ID ABU10486 standard; protein, 304 AA.  
 XX  
 AC ABU10486;  
 XX  
 DT 07-AUG-2003 (first entry)  
 XX  
 DE C-antigen antibody H11 single chain variable region fragment #1.  
 XX  
 KW Human; antibody; H11; single chain variable region; gene therapy; scFv;  
 KW neoplasia; tumour; recurrence risk; C-antigen; melanoma; neuroblastoma;  
 KW glioma; soft tissue sarcoma; small cell lung carcinoma; brain cancer;  
 KW C-antigen specific antibody; alphac; cancer; vaccine.  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 302..303 /note="Encoded by CATTAGTGAAG"  
 FT  
 PN US2003021779-A1.  
 XX  
 PD 30-JAN-2003.  
 XX  
 PF 13-FEB-2001; 2001US-00782397.  
 XX  
 PR 22-MAY-1996; 96US-00657449.  
 PR 22-MAY-1997; 97US-00862124.  
 XX  
 PA (DANM/) DAN M D.  
 PA (MAIT/) MAITI P K.  
 PA (KAPL/) KAPLAN H A.  
 XX  
 PI Dan MD, Maitei PK, Kaplan HA;  
 XX  
 DR WPI; 2003-456278/43.  
 DR N-PSDB; ACA62168; ACA62169.  
 XX  
 PT Novel antigen binding fragment of monoclonal antibody specific for  
 PT antigen detected on neoplastic cells; useful for diagnosing or treating  
 PT cancer, for manufacturing novel reagents and as diagnostic and imaging  
 PT reagent.  
 XX  
 PS Claim 5; Page 34; 62pp; English.  
 XX  
 CC The invention relates to a polypeptide which is an antigen binding  
 CC fragment of a monoclonal antibody specific for an antigen detected on  
 CC neoplastic cells. The antigen binding fragment (ABF) is useful for  
 CC treating a patient with a neoplasia. The individual has a clinically  
 CC detectable tumour. The method is useful for palliating the neoplasia. The  
 CC method reduces the risk of recurrence of a clinically detectable tumour.  
 CC The antigen binding fragment is labelled with a therapeutic moiety such  
 CC as radioisotopes or immunomodulators. ABF is useful for detecting C-  
 CC antigen in a sample. The polypeptide is useful for diagnosing, localising

CC and/or treating neoplasias, including melanoma, neuroblastoma, glioma,  
 CC soft tissue sarcoma and small cell lung carcinoma. The polypeptide is  
 CC useful for manufacturing novel reagents and for treating and imaging  
 CC brain cancer. ABR is useful as a diagnostic and imaging reagent. The  
 CC composition is useful for eliciting an immune response against neoplasia.  
 CC The polynucleotide is useful in expression systems for the production of  
 CC C-antigen specific antibody, termed H11 or alphac, as hybridisation  
 CC probes to assay for the presence of alphac polynucleotide or related  
 CC sequences in a sample, as primers to effect amplification of desired  
 CC polynucleotides and in pharmaceutical compositions including vaccines and  
 CC for gene therapy. The polynucleotide is also useful for genetically  
 CC altering cells in vivo, thus treating various types of cancer. The  
 CC polypeptide, polynucleotide and the composition are useful for detecting  
 CC or treating cancer, including therapy of cancer and prophylactic care,  
 CC particularly for decreasing the risk of recurrence. The present sequence  
 CC represents the amino acid sequence of the human C-antigen specific  
 CC antibody H11 single chain variable region fragment, scFv, #1

XX  
 SQ Sequence 304 AA;

Alignment Scores:  
 Pred. No.: 3.9e-118 Length: 304  
 Score: 1573.00 Matches: 302  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 91.83% Indels: 0  
 DB: 7 Gaps: 0

US-09-194-164-13 (1-918) x ABU10486 (1-304)

QY 1 GAATTCATGTAATAAAACCGGATCGGATCGAGTTCAGTGGCTGTTTCGTACCGTT 60  
 DB 1 GluPheMetLysThrAlaIleAlaValAlaLeuAlaIlyPheAlaThrVal 20  
 QY 61 GCGCAGGCCGAAATTTGTGTGACGAGCTCCAGGCAACCTGTTTCTCCAGGGGAA 120  
 DB 21 AAlaGlnAlaAspIleValLeuThrGlnSerProGlyThrLeuSerLeuSerProGlyGln 40  
 QY 121 AAGAGCCACCTCTCTCGCAGGGGCGGATCGAGTTCAGTTCAGTTCAGTTCAGTTC 180  
 DB 41 ArgAlaThrLeuSerCysArgAlaSerGlnSerValSerSerSerYrLeuAlaTrpYr 60  
 QY 181 CAGCAGAAACCTTGCGGAGGCTCCAGGCTCCATCATGTGTCATCCAGGCGCAGT 240  
 DB 61 GlnGlnLysProGlyAlaIleAlaProGlnLeuLeuIleYrGlyAlaSerThrAlaThr 80  
 QY 241 GGCATCCAGCAGAGGTTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTC 300  
 DB 81 GlyMetProAspArgPheSerGlySerGlyThrAspPheThrLeuThrIleSer 100  
 QY 301 AAGCTGAGACCTGGAATTTTTCAGTTCATGTTCAGTTCAGTTCAGTTCAGTTCAG 360  
 DB 101 ArgLeuGlnProGlnAspPheAlaValYrYrCysGlnGlnIlyGlySerSerProGln 120  
 QY 361 ACACTCAGATCACTTTCGCGGAGGAGCAAGGTGAGATCAAGAACTGTCGCTGCA 420  
 DB 121 ThrProGlnIleThrPheGlyGlyGlyThrLysValGlnIleYrArgThrValAlaAla 140  
 QY 421 CCATCTGTCTTCGCGGCGGCTTCGGAAGTGTGATCAGTTCAGTTCAGTTCAGTTC 480  
 DB 141 ProSerValSerClyGlyGlyGlySerGlyGlyGlySerClyGlyGlyGlySerGln 160  
 QY 481 GTGACACTGTGAGAGTTCGCGGAGGCGTTCGCGGAGGCTTCGCGGAGTTCGCTCC 540  
 DB 161 ValGlnLeuValGlnSerGlyGlyGlyValGlnProGlyArgSerLeuArgLeuSer 180  
 QY 541 TGTGACGCTTCGATTCCTTCAGAACTTTCATGATCAGTTCAGTTCAGTTCAGTTC 600  
 DB 181 CysAlaAlaSerClyPheProPheArgSerPheAlaMetHisTrpValArgGlnAlaLeu 200  
 QY 601 GCGCAGGCGCTGAGTGTGCGTTCAGTTCATGATGAGAACTTAATATCATGCGCA 660  
 DB 201 GlyLysGlyLeuGlnIlyrValAlaValIleSerYrAspGlySerThrIlyrYrAla 220

QY 661 GACTCCGTAAGAGGCGCGATTTCACCATCTTCAGAGACACTTCGAAAGACGGTATCTA 720  
 DB 221 AspSerValLysGlyArgPheThrIleSerArgAspThrSerLysAsnThrValYrLeu 240  
 QY 721 AAAATGAACAGCTGAGAACTGAGAGACAGCGCTGCTATTACTGTGCGAGATCAGAGC 780  
 DB 241 LysMetLanSerLeuArgThrGlnAspThrAlaValYrYrCysAlaArgAspIleSer 260  
 QY 781 CTGTTGGGTGACTATGACCACTACTACGCGTTTGAACGTTCTGGGGGCAAGGACACGCTC 840  
 DB 261 LeuLeuGlyAspYrAspHisTrpYrGlyLeuAspValTrpGlyLysGlyThrThrVal 280  
 QY 841 ACCGCTCTCTCAGGATCCGAAACAAAACTGATCAGCGCAAGAAATCATGACCATCAT 900  
 DB 281 ThrValSerSerGlySerGlnGlnLysLeuIleSerGlnGlnAspLeuAsnHisHis 300  
 QY 901 CACCAT 906  
 DB 301 HisHis 302

RESULT 4  
 AD052296  
 ID AD052296 standard; protein; 304 AA.  
 XX  
 AC AD052296;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Human antibody H11 scFv protein #1.  
 XX  
 KW Antigen binding fragment; H chain V region; L chain V region; C-antigen;  
 XX neoplasia; cancer; vaccine; gene therapy; human;  
 KW single chain V region fragment; scFv.  
 OS Homo sapiens.

Key Location/Qualifiers  
 FH Misc-difference 302..303  
 FT /note="Encoded by CATTCGTGAAAG"

US2004091484-A1.  
 PD 13-MAY-2004.  
 XX  
 PF 29-AUG-2003; 2003US-00651453.  
 XX  
 PR 22-MAY-1996; 96US-00657449.  
 PR 22-MAY-1997; 97US-00862124.  
 PR 13-FEB-2001; 2001US-00782397.

PA (DANM/) DAN M D.  
 PA (MATT/) MATTI P K.  
 PA (KAPL/) KAPLAN H A.  
 PA (GRAD/) GRAD C.  
 PI Dan MD, Matti PK, Kaplan HA, Grad C;

XX  
 DR WPI, 2004-399136/37.  
 DR N-Psdb; AD052295.  
 XX

PT Composition useful for treating neoplasia in patient, comprises antigen  
 PT binding fragment of antibody specifically recognizing C-antigen  
 PT recognized by antibody comprising H chain V region and L chain V region.  
 XX  
 PS Claim 5; SEQ ID NO 14; 56bp; English.

CC The invention relates to a composition comprising an antigen binding  
 CC fragment of an antibody comprising H chain V region and L chain V region  
 CC that specifically recognises C-antigen. The invention is useful for  
 CC treating a patient with a neoplasia. The antigen binding fragment of the  
 CC antibody is used as diagnostic and imaging reagents. The invention is  
 CC useful for genetically altering cells in vivo, to treat various types of





Db 1 GIuphemeLysylbThralaIlealIlealValAlaLeuAlaGlyPheAlaThrVal 20  
QY 61 GGGGAGGCGGATATGTGTGACGAGTCTCCAGGAGCCCTGTCTTGTCTCCAGGGGAA 120  
Db 21 AlaGlnAlaAspIleValLeuThrGlnSerProGlyThrLeuSerLeuSerProGlyGln 40  
QY 121 AAGAGCACCTCTCTGCGAGGGGCGACGTAGAGTGTAAAGACGCTACTTAAGCTGTATC 180  
Db 41 AGGAlaThrLeuSerCysArgAlaSerGlnSerValSerSerSerCysLeuAlaTrpIyr 60  
QY 181 CAGCAGAACTGGCCAGGCTCCAGAGCTCTCATCTATGATGTCATCCAGCGGCCACT 240  
Db 61 GlnGlnLysProGlyGlnAlaProArgLeuIleIleTrpGlyAlaSerThrArgAlaThr 80  
QY 241 GGCATGCGCAGACAGTTTCAGTGGCAGTGGGTCGCGGACAGACTTCACTCCATCACT 300  
Db 81 GlyMetProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSer 100  
QY 301 AAGACTGGAGCTGGAAGATTTTGGAGTGTATTACTGTACAGCATGTATGTAGCTCAGT 360  
Db 101 ArgLeuGlnLysProGlnLysPheAlaValIyrIyrCysGlnGlnIleIyrIyrSerSerProGln 120  
QY 361 AACACCTCAGATCACTTTCGCGGAGGAGGACCAAGGTGAGATCAAAAGAACTGTGGCTGCA 420  
Db 121 ThrProGlnIleThrPheGlyGlyGlyThrLysValGlnIleLysArgThrValAlaAla 140  
QY 421 CCATCTGTCTCTGCGCGTGGCGGTTTCGAGAGTGTGATCAAGTGAAGTGGCTCCAG 480  
Db 141 -----SerglyGln 143  
QY 481 GTGCAGCTGTGGAAGTCTGGGGGAGGCGTGTCCAGCTTGGAGAGTCCCTGAGACTTCC 540  
Db 144 ValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeuSer 163  
QY 541 TTGTGAGCTGTGATTTCCCTTCCAGAACTTGTCTATCATCTGAGTCCGCGAGGCTCTTA 600  
Db 164 CysAlaAlaSerClyPheProPheArgSerPheAlaMetHisTrpValArgGlnAlaLeu 183  
QY 601 GGCAGAGGGCTGAGTGGGTGGCAGTTATATCATATGATGAAGCACTAAATATCTACGCA 660  
Db 184 GlyLysGlyLeuGlnLysPheThrIleSerValAspGlySerThrIyrIyrAla 203  
QY 661 GACTCCGTGAAGGCGGATTCACATCTCCAGAGACTTCCAGAAACGCGGTATCTTA 720  
Db 204 AspSerValLysGlyArgPheThrIleSerArgAspThrSerLysAsnThrValIyrLeu 223  
QY 721 AAAATGAACAGCTGGAAGTGAAGACAGGCTGTCTATTACTGTGCGAGAGTCAAGAC 780  
Db 224 LysMetAsnSerLeuArgThrGlnAspThrAlaValIyrIyrCysAlaArgAspGlnSer 243  
QY 781 CTGTGGGTGACTATGACCACTACACGTTTGGAGCGTCTGGGGCAAGAGGACACGAGTC 840  
Db 244 LeuLeuGlyAspLysArgPheIleIyrIyrGlyLeuAspValTrpGlyLysGlyThrThrVal 263  
QY 841 AACGTTCTCTCGAGATCCGAAACAAACATGATGAGGAGGAAGATCTGAACATCAACCT 900  
Db 264 ThrValSerSerClySerGlnGlnLysLeuIleSerGlnGlnLysPheAsnHisHis 283  
QY 901 CACCAT 906  
Db 284 HisHis 285

RESULT 6  
AAE00948  
ID AAE00948 standard; protein; 287 AA.  
XX  
XX AAE00948;  
XX  
XX 04-JUL-2001 (first entry)  
XX  
XX Human monoclonal antibody H11-single chain variable region (scFv) #2.  
XX

KW Human; monoclonal antibody; Mab; H11; single chain variable region; scFv;  
KW neoplastic disease; melanoma; immunoglobulin IgM; gene therapy; lymphoma;  
KW carcinoma; breast; lung; gastric; prostate; ovary; colon; lung; vaccine;  
KW neuroblastoma; soft tissue sarcoma; prostatic adenocarcinoma; cytostatic;  
KW C-antigen; chronic leukaemia; glioma.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Misc-difference 285..286  
FT /note="Encoded by CATTAAGTGAAG"  
PN US6207153-B1.  
PN 27-MAR-2001.  
XX  
XX 22-MAY-1997; 97US-00862124.  
XX  
XX 22-MAY-1996; 96US-00657449.  
XX  
XX (VIVE-) VIVENTIA BIOTECH INC.  
XX  
XX Dan MD, Maiti PK, Kaplan HA;  
PI  
DR MPI: 2001-289584/30.  
DR N-PSDB; AAD04539.  
XX  
XX Composition comprising antigen binding fragments of an antibody that  
XX recognizes an antigen on neoplastic cells but not on normal cells for use  
XX in diagnosis, imaging and treatment of carcinomas.  
XX  
XX Disclosure: Col 69-70; 56pp: English.  
XX  
XX The present sequence is human monoclonal antibody (Mab), H11-single chain  
XX variable region (scFv). The H11 light chain variable region is linked to  
XX the heavy chain variable region through a (SGGGG)3 linker to form dimers.  
XX The invention relates to human monoclonal antibody (Mab) H11, H11-(scFv)  
XX single chain variable (V) region fragment and their corresponding DNA  
XX molecules. H11 antibody is an immunoglobulin of IgM subclass which is  
XX specific to C-antigen found specifically on neoplastic cells and not on  
XX normal cells. H11 is an antibody obtained from the fusion of peripheral  
XX blood lymphocytes of a 64 year old male with a low grade glioma and fused  
XX to a human myeloma cell line to produce a hybridoma designated NBGM1/H11.  
XX A pharmaceutical composition comprising H11 and its derivatives are  
XX useful in the diagnosis, imaging and treatment of neoplastic disease,  
XX particularly, melanoma, breast carcinoma, lung carcinoma, ovarian  
XX carcinoma, colon carcinoma, gastric carcinoma, prostate carcinoma,  
XX lymphoma carcinoma, neuroblastoma, glioma, soft tissue sarcoma, small  
XX cell lung carcinoma, prostatic adenocarcinoma, B and T cell lymphomas and  
XX chronic leukaemias. H11 DNA is also used in vaccines and gene therapy  
XX  
XX Sequence 287 AA;  
SQ  
XX  
XX Alignment Scores:  
XX Pred. No.: 2,386-108 Length: 287  
XX Score: 1451.50 Matches: 283  
XX Percent Similarity: 93.71% Conservative: 0  
XX Best Local Similarity: 93.71% Mismatches: 2  
XX Query Match: 84.73% Indels: 17  
XX DB: 4 Gaps: 1  
XX  
XX US-09-194-164-13 (1-918) .X AAE00948 (1-287)  
QY 1 GAATTCATGAAAAAAGCGCTTATGCCGATCGCAGTTGCACTGGCTGTTGCTTACCGTT 60  
Db 1 GIuphemeLysylbThralaIlealIlealValAlaLeuAlaGlyPheAlaThrVal 20  
QY 61 GGGGAGGCGGATATGTGTGACGAGTCTCCAGGAGCCCTGTCTTGTCTCCAGGGGAA 120  
Db 21 AlaGlnAlaAspIleValLeuThrGlnSerProGlyThrLeuSerLeuSerProGlyGln 40  
QY 121 AAGAGCACCTCTCTGCGAGGGGCGACGTAGAGTGTAAAGACGCTACTTAAGCTGTATC 180



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Db      41 ArgAlaThrLeuSerCysArgAlaSerGlnSerValSerSerSerTyrLeuAlaTrpTyr 60
QY      181 CAGCGAAACCTGGCGAGCTCCAGGCTCCATCTATATGATGATCCACCGAGGCTCACT 240
Db      61 GlnGlnLysProGlyGlnAlaProArgLeuLeuIleTyrGlyAlaSerThrArgAlaThr 80
QY      241 GGCATGCCAGACAGATTCAGTGGAGGGTCCGGAGACGATTCACCTCCACCATCACT 300
Db      81 GlyMetProAspArgPheSerSerGlySerGlySerGlyThrAspPheThrIleSer 100
QY      301 AGACTGAGAGCTGAAAGATTTTCCAGTGTATTACTGTACAGCACTATGATGATGATGAT 360
Db      101 ArgLeuGlnLysProGlnLysPheAlaValTyrTyrCysGlnGlnTyrGlySerSerProGln 120
QY      361 ACACCTCGATGATCACTTTGGCGGAGGAGACCAAGTGGAGATGAAACGAACTTGCTGTA 420
Db      121 ThrProGlnIleThrPheGlyGlyGlyThrLysValGlnIleLysArgThrValAlaAla 140
QY      421 CCATCTGTCTCTGGCGGTGGCGGTTCCGGAGGTGGTATCAGTGGAGGTGGCTCCGAC 480
Db      141 -----SerGlyGln 143
QY      481 GTGCACTGTGTGAGATCTGGGAGGAGCGCTGTCCAGCTCGGAGGCTCCCTGAGACTCTCC 540
Db      144 ValGlnLeuValGlnSerGlyGlyGlyValValGlnProGlyArgSerLeuArgLeuSer 163
QY      541 TGTGACGCTCTGATTCCTCCCTTCAGAAAGCTTTGCTATGATCACTGGGCTCCGACGCTCTA 600
Db      164 CysAlaAlaSerGlyPheProPheArgSerPheAlaMetIleTrpValArgGlnAlaLeu 183
QY      601 GCGAAGGGGCTGTGAGTGGGTGGGAGCTTATATCATATGATGAAAGCACTAAATACTACGCA 660
Db      184 GlyLysGlyLeuGlnTrpValAlaValIleSerTyrAspGlySerThrLysTyrTyrAla 203
QY      661 GACTCGGTGAAGGCGCATTCACATCTCCAGAGACACTTCCAGAAACGCGTGTATCTTA 720
Db      204 AspSerValLysGlyArgPheThrIleSerArgAspThrIleSerLysAsnThrValTyrLeu 223
QY      721 AAAATGAACAGCTTGAAGATGAGACACGCGTGTCTATTAATCTGTGCGAGAGATCAAGCC 780
Db      224 LysMetAsnSerLeuArgThrGlnAspThrAlaValTyrTyrCysAlaArgAspGlnSer 243
QY      781 CTGTGGGTGACTATGACCACTACACTACGCTTGGAGCTGGGAGGAGCAACGCGTCC 840
Db      244 LeuLeuGlyAspTyrAspIleTyrTyrGlyLeuAspValTyrGlyLysThrVal 263
QY      841 ACCGTCCTCTCAGATCCGAAACAAAATGATCAGCGAAGATCTGACCATCAGCAT 900
Db      264 ThrValSerSerGlySerGlnGlnLysLeuIleSerGlnGlnLysAspLeuAsnIleHis 283
QY      901 CACCAT 906
Db      284 HisHis 285

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## RESULT 7

ABU10487 standard; protein; 287 AA.

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ID      ABU10487
AC      ABU10487;
XX      07-AUG-2003 (first entry)
DT      C-antigen antibody H11 single chain variable region fragment #2.
DE      Human; antibody; H11; single chain variable region; gene therapy; scFv;
XX      neoplasia; tumour; recurrence risk; C-antigen; melanoma; neuroblastoma;
KW      glioma; soft tissue sarcoma; small cell lung carcinoma; brain cancer;
KW      C-antigen specific antibody; alphac; cancer; vaccine.
XX      Homo sapiens.
OS      Synthetic.
XX      Key
XX      Location/Qualifiers

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FT      Misc-difference 285..286
FT      /note="Encoded by CATTACTGAAAG"
FN      US2003021779-A1.
XX      30-JAN-2003.
PD      13-FEB-2001; 2001US-00782397.
XX      22-MAY-1996; 96US-00657449.
PR      22-MAY-1997; 97US-00862124.
XX      (DANM/) DAN M D.
PA      (MATI/) MATI P K.
PA      (KAPL/) KAPLAN H A.
PI      Dan MD, Maiti PK, Kaplan HA,
XX      WPI: 2003-456278/43.
DR      N-PSDB; ACM62170, ACM62171.
XX      Novel antigen binding fragment of monoclonal antibody specific for
PT      antigen detected on neoplastic cells, useful for diagnosing or treating
PT      cancer, for manufacturing novel reagents and as diagnostic and imaging
PT      reagent.
XX      Claim 5; Page 36-37; 62pp; English.
XX      The invention relates to a polypeptide which is an antigen binding
CC      fragment of a monoclonal antibody specific for an antigen detected on
CC      neoplastic cells. The antigen binding fragment (ABF) is useful for
CC      treating a patient with a neoplasia. The individual has a clinically
CC      detectable tumour. The method is useful for palliating the neoplasia. The
CC      method reduces the risk of recurrence of a clinically detectable tumour.
CC      The antigen binding fragment is labelled with a therapeutic moiety such
CC      as radioisotopes or immunomodulators. ABF is useful for detecting C-
CC      antigen in a sample. The polypeptide is useful for diagnosing, localising
CC      and/or treating neoplasias, including melanoma, neuroblastoma, glioma,
CC      soft tissue sarcoma and small cell lung carcinoma. The polypeptide is
CC      useful for manufacturing novel reagents and for treating and imaging
CC      brain cancer. ABF is useful as a diagnostic and imaging reagent. The
CC      composition is useful for eliciting an immune response against neoplasia.
CC      The polynucleotide is useful in expression systems for the production of
CC      C-antigen specific antibody, termed H11 or alphac, as hybridisation
CC      probes to assay for the presence of alphac polynucleotide or related
CC      sequences in a sample, as primers to effect amplification of desired
CC      polynucleotides and in pharmaceutical compositions including vaccines and
CC      for gene therapy. The polynucleotide is also useful for genetically
CC      altering cells in vivo, thus treating various types of cancer. The
CC      polypeptide, polynucleotide and the composition are useful for detecting
CC      or treating cancer, including therapy of cancer and prophylactic care,
CC      particularly for decreasing the risk of recurrence. The present sequence
CC      represents the amino acid sequence of the human C-antigen specific
CC      antibody H11 single chain variable region fragment, scFv, #2
XX      SQ Sequence 287 AA;

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## Alignment Scores:

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Pred. No.: 2,386-108 Length: 287
Score: 1451.50 Matches: 283
Percent Similarity: 93.71% Conservative: 0
Best Local Similarity: 93.71% Mismatches: 2
Query Match: 84.73% Indels: 17
DB: 7 Gaps: 1

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US-09-194-164-13 (1-918) x ABU10487 (1-287)

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QY      1 GAATTCATGAAACAAACCGCTATCGCATTCGAGTTGCTGCTGCTTCCCTACCGTT 60
Db      1 GlnPheMetLysLysThrAlaIleAlaIleAlaValAlaLeuAlaGlyPheAlaThrVal 20
QY      61 GCGCAGCGCGATATGTTGTGACGAGTCTCCAGGACCCCTGCTTGTCTCCAGGGGAA 120

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Db 21 AlaGlnAlaAspIleValLeuThrGlnSerProGlyThrLeuSerLeuSerProGlyGln 40
QY 121 AGAGCCACCTCTCTGCGAGGGCCAGTCAGAGTGTAGTACGACTTACCTGGTAC 180
Db 41 ArgAlaThrLeuSerCysArgAlaSerGlnSerValSerSerSerTyLeuAlaTrpTyr 60
QY 181 CAGGAGAAACCTGGCCAGGCTCCCGAGGCTCCATCTATGAGTATCCACCGAGGCACT 240
Db 61 GlnGlnLysProGlyGlnAlaProArgLeuLeuIleTyGlyAlaSerThrArgAlaThr 80
QY 241 GGCATGCCAGACAGGTTCAGTGAGGAGTCCGGGACAGACTTCACTTCCACATCACT 300
Db 81 GlyMetProAspArgPheSerSerGlySerGlySerGlyThrAspPheThrLeuThrIleSer 100
QY 301 AGACTGAGACCTGAAAGATTTTGCACTGTATTACTGTCAAGATATGATAGCTTCACTCG 360
Db 101 ArgLeuGlnLysProGlyLysPheAlaValTyrCysGlnGlnIleLysArgThrValAlaAla 120
QY 361 ACACCTCAGATCACTTGGCGGAGGACCAAGGTGAGATCAAAACGAACTGGCTGCA 420
Db 121 ThrProGlnIleThrPheGlyGlyGlyGlnTyrValGlnIleLysArgThrValAlaAla 140
QY 421 CCATCTGTCTCGCGGTGGCGGTTCCGAGAGTGTGATCAAGTGAAGTGCCTCCAG 480
Db 141 -----serGlyGln 143
QY 481 GTGCAAGCTGTGAGTCTGGGGAGGCGGTGTCAGCTGGAGAGTCCCTGAGACTTCC 540
Db 144 ValGlnLeuValGlnSerGlyGlyGlyValValGlnProGlyArgSerLeuArgLeuSer 163
QY 541 TGTGAGCCTCTGGAATCCCTTCCAGAACTTGTGATCACTGAGTCCGGTCCGCGAGGCTCA 600
Db 164 CysAlaAlaSerGlyPheProPheArgSerPheAlaMetIleTrpAlaArgGlnAlaLeu 183
QY 601 GCGAAGGGCTGAGTGTGGTGCAGTATATATATATGATGAAAGCACTAAATACTACGCA 660
Db 184 GlyLysGlyLeuGlnTrpValAlaValIleSerTyrAspGlySerThrIleTyrTyrAla 203
QY 661 GACTCCGTGAGAGGGCCGATTACCATCTCCAGAGACACTTCCAAAGAACCGGTATCTTA 720
Db 204 AspSerValLysGlyArgPheThrIleSerArgAspThrSerLysAsnThrValTyrLeu 223
QY 721 AAAATGAACAGCTGAGACGAGTCAAGACAGCGCTATATTACTGTGCGAGATCCAGAC 780
Db 224 LysMetAsnSerLeuArgThrGlnAspTrpAlaValTyrTyrCysAlaArgAspGlnSer 243
QY 781 CTGTTGAGTGAATGACCACTACTACGCTTGGACGTCGCGGCAAGAGCAACGCTC 840
Db 244 LeuLeuGlyAspTrpAspHisTyrTyrGlyLeuAspValTyrGlySerGlyThrThrVal 263
QY 841 ACCGTCCTCTCAGATCCGAAACAAAACCTGATCAGCGAAGAAATCTGAACATCACCAT 900
Db 264 ThrValSerSerGlySerGlnGlnLysLeuIleSerGlyLysAspLeuAsnHisHisHis 283
QY 901 CACCAT 906
Db 284 HisHis 285
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XX Key Location/Qualifiers
FH MISC-difference 285..286
FT /note="Encoded by CATTAGTGAAG"
PN US2004091484-A1.
PD 13-MAY-2004.
PF 29-AUG-2003; 2003US-00651453.
PR 22-MAY-1996; 96US-00657449.
PR 22-MAY-1997; 97US-00862124.
PR 13-FEB-2001; 2001US-00782397.
XX (DANM/) DAN M D.
PA (MALT/) MAITI P K.
PA (KAPL/) KAPLAN H A.
PA (GRAD/) GRAD C.
PI Dan MD, Maite PK, Kaplan HA, Grad C;
XX WPI; 2004-399136/37.
XX N-PSDB; ADO52298.
PT Composition useful for treating neoplasia in patient, comprises antigen
PT binding fragment of antibody specifically recognizing C-antigen
PT recognized by antibody comprising H chain V region and L chain V region.
PS Claim 5; SEQ ID NO 17; 56bp; English.
XX The invention relates to a composition comprising an antigen binding
XX fragment of an antibody comprising H chain V region and L chain V region
XX CC treating a patient with a neoplasia. The antigen binding fragment of the
XX CC antibody is used as diagnostic and imaging reagents. The invention is
XX CC useful for genetically altering cells in vivo, to treat various types of
XX CC cancer. It is also useful in vaccine and gene therapy. The present
XX CC sequence is human antibody H11 single chain V region fragment (scFv).
SQ Sequence 287 AA;
XX Alignment Scores:
Pred. No.: 2,386-108 Length: 287
Score: 1451.50 Matches: 283
Percent Similarity: 93.71% Conservative: 0
Best Local Similarity: 93.71% Mismatches: 2
Query Match: 84.73% Indels: 17
DB: 8 Gaps: 1
US-09-194-164-13 (1-918) x ADO52299 (1-287)
QY 1 GAATTCATGAAAAAACCCTATTCGCGATCGCAGTTGCACTGGCTGGTTGCCCTACCGTT 60
Db 1 GiuphemeTylsYrThrAlaIleAlaIleAlaValAlaLeuAlaGlyPheAlaThrVal 20
QY 61 GCGCAGCGCCGATATGTGTGTGACGAGCTCCAGGCAACCTGTCTTTGTCACAGGAGAA 120
Db 21 AlaGlnAlaAspIleValLeuThrGlnSerProGlyThrLeuSerLeuSerProGlyGln 40
QY 121 AGAGCCACCTCTCTGCGAGGGCCAGTCAGAGTGTAGTACGACTTACCTGGTAC 180
Db 41 ArgAlaThrLeuSerCysArgAlaSerGlnSerValSerSerSerTyLeuAlaTrpTyr 60
QY 181 CAGGAGAAACCTGGCCAGGCTCCCGAGGCTCCATCTATGAGTATCCACCGAGGCACT 240
Db 61 GlnGlnLysProGlyGlnAlaProArgLeuLeuIleTyGlyAlaSerThrArgAlaThr 80
QY 241 GGCATGCCAGACAGGTTCAGTGAGGAGTCCGGGACAGACTTCACTTCCACATCACT 300
Db 81 GlyMetProAspArgPheSerSerGlySerGlySerGlyThrAspPheThrLeuThrIleSer 100
QY 301 AGACTGAGACCTGAAAGATTTTGCACTGTATTACTGTCAAGATATGATAGCTTCACTCG 360
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DB      101 ArgLeuGluProGluAspPheAlaValTyrTyrCysGlnGlnTyrCysSerSerProGln 120
QY      361 ACACTCGATGATCACTTTGGCGGAGGACCAAGGTGGAGATCAAAAGAACTGTGCTGCA 420
DB      121 ThrProGlnIleThrPheGlyGlyGlyThrLysValGluIleLysArgThrValAlaAla 140
QY      421 CCATCTGTCTCTGGGGGTGGCGGTTCCGAGGTGGATCAAGGTGGAGGTGGCTCCGAG 480
DB      141 -----SergLysGln 143
QY      481 GTGAGCTGTGTGAGTCTGGGGAGGCGGTGTCAGCCTGGAGGTCCTTGAGACTCTCC 540
DB      144 ValGlnLeuValGlnSerCysGlyValValGlnProGlyArgSerLeuArgLeuSer 163
QY      541 TGTGAGCCTCTGATATCCCTTCAGAACTTTGCTATGCACTGGGTCGCGCAGGCTCTA 600
DB      164 CysAlaAlaSerGlyPheProPheArgSerPheAlaMetHisTyrValArgGlnAlaLeu 183
QY      601 GGCAAGGGGCTGAGTGGGTGGCACTTATATCATATGATGAAAGCACTTAAATCAACGA 660
DB      184 GlyLysGlyLeuGlnTyrValAlaValIleSerTyrAspGlySerThrLysTyrTyrAla 203
QY      661 GACTCCGTGAAGGGCGGATTCACCATCTCCAGAGACACTTCCAGAAACAGGCTATCTA 720
DB      204 AspSerValLysGlyArgPheThrIleSerArgAspThrSerLysAlaThrValTyrLeu 223
QY      721 AAATGAACAGCCTGAGAACTGAGGACACGCGTCTATTACTGTGCGAGATCAGAGC 780
DB      224 LysMetCAnSerLeuArgThrGlnAspThrAlaValTyrTyrCysAlaArgAspGlnSer 243
QY      781 CTGTTGGGTGATATGACACACTACTACGTTTGGACGTTGGGGGCAAGGGACACGCGTC 840
DB      244 LeuLeuGlyAspTyrAspHisTyrTyrGlyLeuAspValTyrGlyLysGlyThrThrVal 263
QY      841 ACCGTCCTCGATGATCCGACAAACAAATGATCAGGAAAGATCTGAACATCAGCATC 900
DB      264 ThrValSerSerGlySerGlnGlnLysLeuIleSerGlnGlnAspLeuMetHisHis 283
QY      901 CACCAT 906
DB      284 HisHis 285

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XX      XX (PROC-) PROCHON BIOTECH LTD.
PA      Yavon A, Rom E;
XX      WPI, 2003-175236/17.
XX      N-PsDB; ADA89102.
PT      New antibodies which have specific binding affinity for a receptor
PT      protein tyrosine kinase (RPTK) and block constitutive activation of RPTK,
PT      useful for treating bone and cartilage disorders, or malignant cell
PT      proliferative diseases.
PS      Example 3; Fig 29B; 122pp; English.
XX      XX
XX      XX The present invention describes a molecule (I) comprising the antigen
XX      XX binding portion of an isolated antibody which has specific binding
XX      XX affinity for a receptor protein tyrosine kinase (RPTK), particularly for
XX      XX a fibroblast growth factor receptor (FGFR), and which blocks constitutive
XX      XX activation of an RPTK. Also described: (1) pharmaceutical compositions
XX      XX comprising (I) as an active ingredient and a pharmaceutical carrier,
XX      XX excipient, or auxiliary agent; (2) a kit comprising (1), at least one
XX      XX reagent for detecting the presence of (1) when bound to the RPTK, and
XX      XX instructions for use; (3) a method for treatment of bone and cartilage
XX      XX related disorders by administering a composition of (1) to the subject;
XX      XX (4) a method for treating or inhibiting a cell proliferative disease or
XX      XX disorder by administering the composition of (1); (5) a method for
XX      XX screening a molecule comprising the antigen-binding portion of an
XX      XX antibody which blocks ligand-dependent activation of RPTK; (6) an
XX      XX isolated nucleic acid molecule encoding a VL-CDR3 DNA region and a VH-
XX      XX CDR3 DNA region; (7) an isolated nucleic acid molecule encoding VL region
XX      XX and a VH region; (8) vectors comprising a nucleic acid molecule of (6) or
XX      XX (7); and (9) host cells transformed with the vector. (I) have
XX      XX osteopapthic, cytoskeletal and ophthalmological activities, and can be used
XX      XX as a RPTK inhibitor. Compositions comprising (I) are useful for treating
XX      XX bone and cartilage disorders, including skeletal disorders such as
XX      XX skeletal dysplasia (achondroplasia, chondroplasia, chondrodysplasia,
XX      XX hypochondroplasia, severe achondroplasia with developmental delay and
XX      XX acanthosis nigricans dysplasia) or a craniosynostosis disorder (e.g.,
XX      XX Muenke coronal craniosynostosis or Crouzon syndrome with acanthosis
XX      XX nigricans). The composition may also be used for treating or inhibiting
XX      XX malignant cell proliferative disease or disorder associated with abnormal
XX      XX RPTK activity, including a hematopoietic malignancy (e.g., multiple
XX      XX myeloma), solid tumors (e.g., mammary, colon, cervical, bladder,
XX      XX colorectal, chondrosarcoma or osteosarcoma), tumour formation, primary
XX      XX tumours, tumour progression (particularly progression of transitional
XX      XX cell carcinoma or mammary carcinoma), or tumour metastasis, where the
XX      XX cell proliferative disorder may be associated with the action of a
XX      XX constitutively activated RPTK, or with ligand-dependent activation of
XX      XX RPTK. The compositions may further be used for treating
XX      XX hyperproliferative diseases and disorders associated with ligand-
XX      XX dependent FGFR signaling, such as vision disorders (e.g., neovascular
XX      XX glaucoma, macular degeneration and proliferative retinopathy including
XX      XX diabetic retinopathy), and non-neoplastic angiogenic pathologic
XX      XX conditions (e.g., haemangiomas, angiodiomas and psoriasis). The present
XX      XX sequence is given in the exemplification of the present invention.
XX      XX
SQ      Sequence 638 AA;

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Alignment Scores:
Pred. No.: 3e-73
Score: 1016.50
Percent Similarity: 61.86%
Best Local Similarity: 57.99%
Query Match: 59.34%
DB: 6
Gaps: 5

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US-09-194-164-13 (1-918) x ADA89103 (1-638)
QY      7 ATGAAAAAACCGCTATCGCATGCGATTCGATGCGTGGTTGCTACCGTTGCGAG 66
DB      1 MetLysLysThrAlaIleAlaIleAlaValAlaLeuAlaGlyPheAlaThrValAlaGln 20

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QY	67	GGCGAATATTGGTTGACGAGCTCCAGGACCCCTGCTTTGGTCCAGGGGAAAGGCC	126
Db	21	AlaAspIleValLeuThrGlnSerProAlaThrLeuSerLeuSerProGlyGluAla	40
QY	127	ACCCCTCCTGACGAGGCCAGTCCAGAGTGTTAGTAGAGCTACTTAGCTGTGACAG	186
Db	41	ThrLeuSerCysArgAlaSerGlnSerValSerSerSerLeuAlaTrpGlnGln	60
QY	187	AAACCTGSCCAGGCTCCAGGCTCCATCTATGTGTCATCCACAGGGCCACTGGCATG	246
Db	61	LysProGlyGlnAlaProArgLeuLeuIleTyrGlyAlaSerSerArgAlaThrGlyVal	80
QY	247	CCAGACAGGTTGACGTGGCGATGGGTCGGGACAGACTTCCTCCATCCATCAGTAAGCTG	306
Db	81	ProAlaArgPheSerSerIleSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu	1000
QY	307	GAGCTGGAAGATTTTGGTCAGTGTATTACTGTCAGACAGATGTAGTCACTCCACAGACACT	366
Db	101	GluProGluAspPheAlaValTyrTyrCysGlnGlnIleSerThrThrProPro-----	118
QY	367	CAGATCATCTTTGGCGGAGGACCAAGGTGAGATCAACGAACGTGGCTGCAACATCT	426
Db	119	-----ThrPheGlyGlnGlyThrLysValGluIleLysArgThrValAlaAlaProSer	136
QY	427	GTC-----	429
Db	137	ValPheIlePheProProSerAspGlnGlnLeuLysSerGlyThrAlaSerValCys	156
QY	429	-----	429
Db	157	LeuLeuAsnAsnPheTyrProArgGluAlaLysValGlnTrpLysValaAspAsnAlaLeu	176
QY	430	---TCTGGC-----	435
Db	177	GlnSerGlyAsnSerGlnGlnSerValThrGlnGlnAspSerLysAspSerThrTyrSer	196
QY	435	-----	435
Db	197	LeuSerSerThrLeuThrLeuSerLysValaAspTyrGluLysHisLysValTyrAlaCys	216
QY	436	-----GGTGGCGGTCCCGAGGTGGTGATCAGGTGGAGAGTCCCTGAGA	474
Db	217	GluValThrHisGlnGlyLeuSerSerProValThrLysSerPheAsnArgGlyGluAla	236
QY	474	-----	474
Db	237	MethylGlnSerThrIleAlaLeuAlaLeuLeuProLeuLeuPheThrProValThrLys	256
QY	475	TCCCAAGTCCAGCTGGTGAAGTCTGGGGGAGCGCTGTCACAGCTGGGAGAGTCCCTGAGA	534
Db	257	AlaGlnValGlnLeuValaGlnSerGlyGlyGlyLeuValGlnProGlyGlySerLeuArg	276
QY	535	CTCTCCTGTCAGGCTCTGGATTCCCTTCAGAAAGCTTTGCTTAATGCACTGGTCCCGCAG	594
Db	277	LeuSerCysAlaAlaSerGlyPheThrPheSerSerTyrAlaMetSerTrpValaGln	296
QY	595	GCTTAGGCAAGGGCTGAGTGGGTGGCGAGTTATATCATATGATGAGACACTAAATAC	654
Db	297	AlaProGlyLysGlyLeuGlnTrpValSerAlaIleSerGlySerGlyLysSerThrTyr	316
QY	655	TACGCAAGACTCCGTGAAGGGCCGATTACATCTCCAGAGACACTTCGAAGAACCGGTG	714
Db	317	TyrAlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu	336
QY	715	TATCTAAATAATGAACGCTGAGACACTGAGACACAGCGCTGTATTACTGTGGAGAGAT	774
Db	337	TyrLeuGlnMetAsnSerLeuAlaGlnAlaAspThrAlaValTyrTyrCysAlaArg---	355
QY	775	CAGAGCTGTTGGGTACTATGACCACTACTAGCTGTGGACGCTGGGCAAGGAGACC	834
Db	356	-----TrpIleGlyAlaProGlyPheTyrAlaMetAspTyrTrpIleGlyGlnGlyThr	371
QY	835	ACGGTCACCGTCTCTCAGAGATCC	858

Db 372 LeuValThrValSerSerLeuAsp 379  
|||  
RESULT 10  
ID ADA90139 standard; protein; 638 AA.  
XX ADA90139  
AC ADA90139;  
XX 20-NOV-2003 (first entry)  
DT Anti-Abeta antibody related amino acid sequence SEQ ID NO:254.  
DE  
XX antiobody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective;  
KW neurotrophic; antiparkinsonian; gene therapy; amyloidogenesis;  
KW Alzheimer's disease; motor neuropathy; Down's syndrome;  
KW Alzheimer's disease; motor neuropathy; Down's syndrome;  
KW Cretzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis;  
KW Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;  
KW neuronal disorder; aging.  
OS Synthetic.  
OS Homo sapiens.  
XX MO2003070760-A2.  
PM 28-AUG-2003.  
PD 20-FEB-2003; 2003MO-EP001759.  
PF 20-FEB-2002; 2002EP-00003844.  
PR 20-FEB-2002; 2002EP-00003844.  
XX  
XX (HOFF ) HOFFMANN IA ROCHE & CO AG F.  
PA (MORP-) MORPHOSYS AG.  
XX  
PI Bardehoff M, Bohrmann B, Brockhaus M, Huber W, Kretschmar T;  
PI Loehning C, Loetscher H, Nordstedt C, Roche C;  
DR WPI; 2003-663848/62.  
XX  
XX New antibody molecule capable of specifically recognizing two regions of  
PT the beta-A4 peptide, useful for diagnosing, preventing or treating  
PT diseases associated with amyloidogenesis or amyloid-plaque formation  
PT (e.g. dementia).  
XX  
PS Disclosure; Page 251-254; 312pp; English.  
XX  
XX The present invention describes an antibody molecule (I) capable of  
CC specifically recognising two regions of the beta-A4 peptide/Abeta4. The  
CC first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-  
CC Ser-Gly-Tyr AD898986 or its fragment, and the second region comprises the  
CC Glycine acid sequence Val-Ile-His-Gln-Lys-Phe-Val-Phe-Ala-Glu-Asp-Val-  
CC Glny AD898987 or its fragment. Also described: (1) a nucleic acid molecule  
CC encoding (1); (2) a vector comprising the nucleic acid of (1); (3) a host  
CC cell comprising the vector of (2); (4) preparing (1), comprising  
CC culturing the host cell of (3) under conditions that allow synthesis of  
CC (1) and recovering (1) from the culture; (5) a composition comprising (1),  
CC or an antibody molecule produced by method (4); (6) a kit comprising (1),  
CC nucleic acid of (1), vector of (2) or host cell of (3); (7) optimising  
CC (1); (8) testing the resulting Fab optimisation library by panning  
CC against Abeta4/Delta4; (9) identifying optimised clones; (10) expressing  
CC composition, comprising optimisation of (1), and formulating the  
CC optimised antibody/antibody molecule with a carrier; and (12) a  
CC pharmaceutical composition prepared by method (8). (1) has  
CC neuroprotective, neurotropic and antiparkinsonian activities, and can be  
CC used in gene therapy. The antibody molecule (I), nucleic acid molecule,  
CC vector or host is useful in preparing a pharmaceutical composition for  
CC the prevention and/or treatment of a disease associated with  
CC amyloidogenesis and/or amyloid-plaque formation. The antibody molecule  
CC may also be used in preparing a diagnostic composition for the detection  
CC of the disease mentioned above. The antibody is used for the  
CC diagnosis of beta-amyloid plaques or for passive immunisation

CC against beta-amyloid plaque formation. In particular, the disease is  
 CC dementia, Alzheimer's disease, motor neuropathy, Down's syndrome,  
 CC Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with  
 CC amyloidosis Dutch type, Parkinson's disease, HIV-related dementia,  
 CC amyotrophic lateral sclerosis or neuronal disorders related to aging. The  
 CC present sequence is used in the exemplification of the present invention.

XX Sequence 638 AA:

Alignment Scores:

Pred. No.:	3e-73	Length:	638
Score:	1016.50	Matches:	225
Percent Similarity:	61.864	Conservative:	15
Best Local Similarity:	59.994	Mismatches:	35
Query Match:	59.348	Indels:	113
DB:	6	Gaps:	5

US-09-194-164-13 (1-918) x ADA90139 (1-638)

```

QY 7 ATGAAAAAACCCTATCCCGATCGAGTTGCACTGGCTGTTGCTACCGTTGGCGAG 66
DB 1 MetLysLysThrAlaIleAlaIleAlaValAlaLeuAlaGlyPheAlaThrValAlaGln 20
QY 67 GCCGATATTGTGTGAAGAGTCTCCAGGACACCCCTGTTGTTGTCAGAGGAAAGAGCC 126
DB 21 AlaAspIleValIleuThrGlnSerProAlaThrLeuSerLeuSerProGlyGlnAla 40
QY 127 ACCCTCTCTGAGAGGCGCAGTCAGAGTGTAGAGCACTAGTACCTGTGTACAGCAG 186
DB 41 ThrLeuSerCysAlaGlnSerGlnSerValSerSerSerTyrLeuAlaIleThrGlnGln 60
QY 187 AAACCTGGCAGAGCTCCAGGCTCTCATCTATGTGTGATCCACCGGGCCACTGGCATG 246
DB 61 LysProGlyGlnAlaProAlaProGlnLeuLeuIleTyrGlyAlaSerSerAlaThrGlyVal 80
QY 247 CCAGACAGGTTGAGTGGCAGTGGGTCCTCCGGGACAGACTTCACTCTGACATGAGACTG 306
DB 81 ProAlaArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100
QY 307 GAGCTGAAGATTTTGGACGTATTAATCTGTACAGCATAGTATGATGACCTCAGACACCT 366
DB 101 GlnProGlnLysPheAlaValTyrTyrCysGlnGlnIleTyrThrProPro----- 118
QY 367 CAGATCACTTTGGCGGAGGAGCAAGAGTGAAGATAAAGAACTGTGGCTGCACCATTT 426
DB 119 -----ThrPheGlyGlnGlyThrLysValGlnIleLysArgThrValAlaIleProSer 136
QY 427 GTC----- 429
DB 137 ValPheIlePheProProSerAspGlnLeuLysSerGlyThrAlaSerValValCys 156
QY 429 ----- 429
DB 157 LeuLeuAsnAsnPheTyrProArgGlnAlaLysValGlnThrLysValAlaAspAsnAlaLeu 176
QY 430 ----TGTGGC----- 435
DB 177 GlnSerGlyAsnSerGlnGlnSerValThrGlnAspSerLysAspSerThrTyrSer 196
QY 435 ----- 435
DB 197 LeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlnLysIleLysValTyrAlaCys 216
QY 436 -----GTTGGCGGTTCCCGAGGTGGTGAATCAGTGAAGTGGC----- 474
DB 217 GluValThrAspGlnGlnLysLeuSerSerProValThrLysSerPheAsnArgLysGlnAla 236
QY 474 ----- 474
DB 237 MetLysGlnSerThrIleAlaLeuAlaLeuLeuProLeuLeuPheThrProValThrLys 256
QY 475 TCCCAAGTTCAGACTGGTGAATCTGGGGGAGCGTGTGTCAGCTGGAGAGTCCCGTGA 534
  ::::::::::::::::::::::::::::::::::::::::::::::::::::
  
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DB 257 AlaGlnValGlnLeuValGlnSerGlyGlyGlyLeuValGlnProGlyLysLeuArg 276
QY 535 CTCTCTGTGACAGCTCTGGGATTTCCCTTCAGAAAGTTTGTAATGACATGGGTCGCGAG 594
DB 277 LeuSerCysAlaAlaSerGlyPheThrPheSerSerTyrAlaMetSerTyrValArgGln 296
QY 595 GCTCTAGCAAGAGGGCTGAGAGTGGTGGCAGTTATATCATATGATGAGCAACTAAATTC 654
DB 297 AlaProGlyLysGlyLeuGlnIleThrValSerAlaIleSerGlySerGlySerThrTyr 316
QY 655 TACGAGACTCCGTAAGAGGCGCATTCACATCTCCAGAGACACTTCCAGAAACAGGAG 714
DB 317 TyrAlaAspSerValLysGlyLysArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 336
QY 715 TATCTTAAATGAACAGCTTGAGAACTGAGACACGCGTGTCTATTACTGTGGAGAGAT 774
DB 337 TyrLeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyrCysAlaArg--- 355
QY 775 CAGACCTCTGTGGTGATATGACCACTACTACGCTTGGAGCTCTGGGGCAAGGAGAC 834
DB 356 -----TyrGlyGlyAspGlyPheTyrAlaMetAspLysTyrGlyGlnGlyThr 371
QY 835 ACGTCAACGCTCTCTCAGATCC 858
DB 372 LeuValThrValSerSerAlaSer 379

RESULT 11
ADA91410
ID ADA91410 standard; protein; 638 AA.
XX
XX ADA91410;
XX
XX 20-NOV-2003 (first entry)
DT
XX
XX DE
XX Anti-Abeta antibody related amino acid sequence #8.
XX
XX antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective;
XX neurotropic; antiparkinsonian; gene therapy; amyloidogenesis;
XX Alzheimer's disease; motor neuropathy; Down's syndrome;
XX Alzheimer's disease; motor neuropathy; Down's syndrome;
XX Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis;
XX Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
XX neuronal disorder; aging.
XX
XX Synthetic.
XX OS Homo sapiens.
XX
XX PN MO2003070760-A2.
XX
XX PD 28-AUG-2003.
XX
XX PF 20-FEB-2003; 2003WO-EP001759.
XX
XX PR 20-FEB-2002; 2002EP-00003844.
XX
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX (MORP-) MORPHOSYS AG.
XX
XX PI Bardeff M, Bohrmann B, Brockhaus M, Huber W, Kretschmar T;
XX Loehning C, Loetscher H, Nordstedt C, Roche C;
XX
XX WPI; 2003-663848/62.
XX
XX New antibody molecule capable of specifically recognizing two regions of
XX the beta-A4 peptide, useful for diagnosing, preventing or treating
XX diseases associated with amyloidogenesis or amyloid-plaque formation
XX (e.g. dementia).
XX
XX Example 1; Fig 2; 312pp; English.
XX
XX The present invention describes an antibody molecule (I) capable of
XX specifically recognising two regions of the beta-A4 peptide/Abeta4. The
XX first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-
  
```

Seq-GlycYr ADA89886 or its fragment, and the second region comprises the amino acid sequence Val-His-His-Gln-Lys-Ileu-Val-Phe-Ala-Gln-Asp-Val-Gly ADA89887 or its fragment. Also described: (1) a nucleic acid molecule encoding (1); (2) a vector comprising the nucleic acid of (1); (3) a host cell comprising the vector of (2); (4) preparing (1), comprising culturing the host cell of (3) under conditions that allow synthesis of (1) and recovering (1) from the culture; (5) a composition comprising (1) or an antibody molecule produced by method (4); (6) a kit comprising (1), nucleic acid of (1), vector of (2) or host cell of (3); (7) optimising (1); (8) testing the resulting Fab optimisation library by panning against Abeca/Abeta4; (9) identifying optimised clones; (10) expressing of selected, optimised clones; (11) preparing a pharmaceutical composition, comprising optimisation of (1), and formulating the optimised antibody/antibody molecule with a carrier, and (12) a pharmaceutical composition prepared by method (8). (1) has neuroprotective, neurotropic and antiparkinsonian activities, and can be used in gene therapy. The antibody molecule (1), nucleic acid molecule, vector or host is useful in preparing a pharmaceutical composition for the prevention and/or treatment of a disease associated with amyloidogenesis and/or amyloid-plaque formation. The antibody molecule may also be used in preparing a diagnostic composition for the detection of the disease mentioned above. The antibody is used for the disintegration of beta-amyloid plaques or for passive immunisation against beta-amyloid plaque formation. In particular, the disease is dementia, Alzheimer's disease, motor neuropathy, Down's syndrome, Creutzfeldt Jakob disease, hereditary cerebral haemorrhage with amyloidosis Dutch type, Parkinson's disease, HIV-related dementia, amyotrophic lateral sclerosis or neuronal disorders related to aging. The present sequence is used in the exemplification of the present invention.

**SQ** Sequence 638 AA;

Alignment Scores:	
Pred. No.:	3e-73
Score:	1016.50
Percent Similarity:	61.86%
Best Local Similarity:	57.99%
Query Match:	59.34%
DB:	6
Length:	639
Matches:	22
Conservative:	15
Mismatches:	35
Indels:	113
Gaps:	5

US-09-194-164-13 (1-918) X ADA91410 (1-638)

[illegible]

QY	429	429	-----	429
Db	157	LeuLeuAaNsApNheTyRProArGlUaLAlYsValGInTrPlySValAspAmaLaLeu	176	
QY	430	----TCTGGC-----	435	
Db	177	GlInSerClYAsnSerGlInuSerValThrGlInuInAspSerLyAspSerThrTySer	166	
QY	435	-----	435	
Db	197	LeuSerSerThrLeuThrLeuSerLySAlAspTyRGlulYShLsLySValTyRAlaCys	216	
QY	436	-----GGTGGCGGTTCCGGAGGTGGTGAATCAGGTGGAGGTGGC-----	474	
Db	217	GlUValThrHISelInGInLyLeuSerProValThrLySbSerPheAmaRglYGlUAla	236	
QY	474	-----	474	
Db	237	MetLySglInSerThrLLeuLaLeuLeuPProLeuLeuPheThrProValThrLyS	256	
QY	475	TCCAGAGTGACGTGGTGGAGTCTTGGGGAGCGGTGTCACGCTGGGAGGTCCCTGAGA	534	
Db	257	AlaGlInValGInLeuValGlInSerGlYglYglYLeuValGInProGlYglYSerLeuArg	276	
QY	535	CTCTCCCTGGACGCTCGTGGATTTCCCTTCAGAAAGCTTGATGACCTGGGTCGGCAG	594	
Db	277	LeuSerCyAlaAlaSerLyPheThrPheSerSerTyRAlaMetSerTrpValArgGln	296	
QY	595	GCTCTTAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGGAAAGCACTAAATAC	654	
Db	297	AlaProGlYlySelyLeuGlInuTrPAlSerAlaIleSerLySerGlYglYSerThrTyR	316	
QY	655	TAGCGAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACACTTCCAGAAACAGGTG	714	
Db	317	TyRAlAspSerValYlSelyArpPheThrLLeSerArpAspAsnSerLyAsnThrLeu	336	
QY	715	TATCTAAATATGAACAGCTGAGACTGAGACCTAGAGACACGGCTGCTTATCTGTGCGAGAGAT	774	
Db	337	TyLeuGlnMeChsSerLeuArpAlaGlnAspThrAlaValTyRtyCysAlaArg---	355	
QY	775	CAGAGCCTGTGGGTGACTATGACCACTACGAGTTTGAACGTCTGGGGCAAGGACCC	834	
Db	356	-----TrrpGlYglYAspGlYlyPheTyRAlaMetAspTyRTrpGlYglInGlyThr	371	
QY	835	ACCGTACCCGCTCTCTCTCAGAGATCC	858	
Db	372	LeuValThrValSerSerAlaSer	379	
RESULT 12				
ADG74355				
ID ADG74355 standard; protein; 747 AA.				
ADG74355;				
11-MAR-2004 (first entry)				
MSPRO Light chain variable region protein, SEQ ID No 92.				
antigen binding; receptor protein tyrosine kinase;				
fibroblast growth factor receptor 3; FGFR3; osteopontin; cytoskeletal;				
neurotrophic; neuroprotective; ophthalmological; anti-diabetic; gene therapy;				
bone; cartilage; cranioynostosis; skeletal dysplasia;				
cell proliferative disorder; haematopoietic malignancy;				
hyperproliferative disorder; neurovascular glaucoma;				
macular degeneration; proliferative retinopathy; diabetic retinopathy;				
MSPRO.				
Unidentified.				
W02002102972-A2.				
27-DEC-2002.				

Db	210	GIuPProGluAaPheAlaValTyrTyrCyGInGlnHiIeTyrThrThrProPro-----	22
QY	367	CAGATCACTTTCGGCGGAGGGAACCAAGGTGGAGATCAACGAACGTGGCTGCACCATCT	422
Db	228	-----ThrPheGlyGlnGlyThrLysValGluIleLysArgThrValAlaAlaProSer	245
QY	427	GTC-----	422
Db	246	ValPheIlePheProProSerAaPcGluGlnLeuLysSerGlyThrAlaSerValValCys	265
QY	429	-----	422
Db	266	LeuLeuAaAaPhePheTyrProArgGluAlaLysValGlnTrpLysValAlaAaAaAlaLeu	285
QY	430	---TCTGGC-----	435
Db	286	GlnSerGlyAaAaSerGlnGlnSerValThrGlnGlnAaSerLysAaPheSerThrTyrSer	305
QY	435	-----	435
Db	306	LeuSerSerThrLeuThrLeuSerLysAlaAaPyrGluLysHisLysValTyrAlaCys	325
QY	436	-----GGTGGCGGCTCCCGAGAGGGGTGGATCAGGTGGAGGTGGC-----	474
Db	326	GluValThrHisGlnGlyLeuSerSerProValThrLysSerPheAaAaArgLysGluAla	345
QY	474	-----	474
Db	346	MetyLysGlnSerThrIleAlaLeuAlaLeuLeuProLeuLeuPheThrProValThrLys	365
QY	475	TCCCAAGGTGACAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCTGGAGAGTCCCTGAGA	534
Db	366	AlaGlnValGlnLeuValGlnLysSerGlyLysLeuValGlnProGlyLysSerLeuArg	385
QY	535	CTCTCCGTGGACGCTCGATGATTCCTCCCTCAGAAAGCTTGCTATAGACAGCGTCCGCGCAG	594
Db	386	LeuSerCysAlaAlaSerGlyPheThrPheSerSerTyrAlaMetSerTrpValArgGln	405
QY	595	GCTCTAGGCAAGGGGCGTGGAGTGGGTGCGAGTTATATCATGATGGAAGCACTAAATAC	654
Db	406	AlaProGlyLysGlyLeuGlnLutrpAlaSerAlaIleSerGlySerLysGlnSerThrTyr	425
QY	655	TACGCAAGCTCCGTGAAGGGCCGATTCACCATCTCCAGAGACACTTCCAGAAACAGCGTG	714
Db	426	TyrAlaAaPseValLysGlyArgPheThrIleSerArgAaPseAaSerLysAaThrLeu	445
QY	715	TATCTAAATAAAGAACAAGCTCGAAGACTGAGAGACAGCGCTGTCTATATCTGTGGAGAGAT	774
Db	446	TyrLeuGlnMetAaAaSerLeuArgAlaGluAaPThrAlaValTyrLysCysAlaArg--	464
QY	775	CAGAGCTGTGGGAGACTATGACACACTACTACGGTTGTGGACGTGGGGAAGGAGCC	834
Db	465	-----TrpGlyGlyAaPcGlyPheTyrThrAlaMetAaPTrpTrpGlyGlnGlyThr	480
QY	835	ACGGTCACCGTCTCTCAGGATCC	858
Db	481	LeuValThrValSerSerAlaSer	488
RESULT 13			
AAAY44994			
Id	AAAY44994	standard; protein; 523 AA.	
AAAY44994;			
DE	23-MAY-2000	(first entry)	
DE	HD70bCFV-CH1-GM-CSF chain.		
KM	HD70; single-chain variable fragment; scFv; 17-1A antigen; human; EpcAM;		
KM	epithelial cell adhesion molecule; inflammatory cytokine; GM-CSF;		
KM	granulocyte/macrophage colony stimulating factor; heteroantibody;		
KM	CH1-domain; multifunctional compound; heavy chain constant domain;		
KM	immunoglobulin; cytostatic; immunostimulatory; anti-leukemia; diagnosis;		



XX	antiproliferative; prevention; treatment; malignant; haematopoietic cell;
KW	Lymphoma; leukaemia; solid tumour; carcinoma; melanoma; sarcoma.
XX	
XX	Homo sapiens.
XX	
XX	WO200006605-A2.
XX	
XX	10-FEB-2000.
XX	
XX	28-JUL-1999; 99WO-EP005416.
XX	
XX	28-JUL-1998; 98EP-00114082.
XX	
XX	(MIGR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.
XX	
XX	Kufer P, Dreier T, Baewerle PA, Borschert K, Zettl F;
XX	WPI, 2000-195265/17.
DR	N-PSDB; AA250587.
XX	
XX	New multifunctional compounds useful for preventing and/or treating
XX	malignant cell growth and for detection and diagnosis.
XX	
XX	Example 10; Fig 55A, 166pp; English.
XX	
XX	The patent discloses heteroninobodies which are multifunctional compounds
CC	producible in a mammalian host cell as a secretable and fully functional
CC	heterodimer of two polypeptide chains, where one of the polypeptide
CC	chains comprises, a CH1-domain (constant domain of an immunoglobulin
CC	heavy chain) and the other chain comprises C $\mu$ -domain (constant domain of
CC	an immunoglobulin light chain). The polypeptide chains further comprise,
CC	fused to the constant domains at least two (polypeptides having
CC	different receptor or ligand functions, where further at least two of the
CC	different (polypeptides lack an intrinsic affinity for one another and
CC	are linked via the constant domains. The heteroninobodies have
CC	cytostatic, immunostimulatory, antileukaemia and antiproliferative
CC	activities. These compounds can be used for diagnosing, preventing and
CC	treating malignant cell growth related to malignancies of haematopoietic
CC	cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,
CC	melanomas and sarcomas. The present sequence is the left chain of a
CC	heteroninobody comprising HD70 single-chain Fv (scFv) fragment N-
CC	terminally linked to human CH1 domain which bears at its C-terminus the
CC	human inflammatory cytokine granulocyte/macrophage colony stimulating
CC	factor (GM-CSF), plus a hexahistidine sequence for ease of purification.
CC	HD70 scFv specifically recognises the human epithelial cell adhesion
CC	molecule (EPCAM) also called 17-1A antigen
XX	
XX	Sequence 523 AA;
XX	
XX	Alignment Scores:
XX	
XX	Pred. No.: 8,34e-71 Length: 523
XX	Score: 986.00 Matches: 193
XX	Percent Similarity: 80.65% Conservative: 32
XX	Best Local Similarity: 69.18% Mismatches: 38
XX	Query Match: 57.56% Indels: 16
XX	DB: 3 Gaps: 4
XX	
XX	US-09-194-164-13 (1-918) x AAY44594 (1-523)
QY	28 ATCGAGATTGACATGGCTGGTTTCGCTACCGTTGCCAGGCCGATATTGTTGACGACG 87
DB	6 IIEIIeLeuPheLeuValAlaThrAlaThrGlyValHisSerGluLeuGlnMetThrGln 25
QY	88 TCTCCAGGACCCCTGTCCTTTGTCCTCCAGGGGAAGAAGCCACCCCTCTCCAGAGGCAGT 147
DB	26 SerProSerSerLeuSerLeuSerValGlyAspArgValThrIleThrCysArgAlaSer 45
QY	148 CAGAGTGTATGTATGACGCTACTTAGCCTGGTACACAGAGAAGAACTGGCCAGGCTCCAGG 207
DB	46 GlnSerIle---SerSerIyrLeuAenIrrPyrGlnGlnIlySerProGlyGlnProIlyls 64
QY	208 CTCCTCATCTATGTGTCATCCACACAGGACCACTGGCAGATGCCAAGAGTTCAGTGGCAGT 267

Db	65	LeuLeu1e1YrTrpAlaSerThrArgLysSerGlyValProAspArgPheSerGlySer	84
Qy	268	GGGTCGCGGAGACAGACTTCACCTCTCCACATCAGTAGACCGTGAAGATTTTGCACTG	327
Db	85	GlusErGlyThrAsnTyrThrLeuThrIleSerSerLeuGlnProGluAspPheAlaThr	104
Qy	328	TATTACTGTCCAGCATGATGTAAGCTCACCTCAGACACCTCAGATCACTTTCGGCGGAGG	387
Db	105	TyrPheCysGlnGlnSerAspSerLeuPro-----IleThrPheGlyGlnGly	120
Qy	388	ACCAAGAGAGAGATCAACAGAACTGTGCTGCACCATCTGTCTCTGCGGCGGTTCC	447
Db	121	ThrArgLeuAspIleGln-----GlyGlyGlyGlySer	131
Qy	448	GGAGGTGTGTGATCAGGTGAGAGTGTCTCCAGGTGCAGGTGTGAGAGTCTGGGAGGCG	507
Db	132	GlyGlyGlyGlySerGlyGlyGlyGlySerGluValGlnLeuLeuGlnSerGlyGlyGly	151
Qy	508	GTGTGTCCAGCTGGGAGGCTCCCTGAGACTCTCTCTGTGCAAGCTCTTGGAATCCCTTCA	567
Db	152	ValValGlnProGlyArgSerLeuArgLeuSerCysAlaAlaSerGlyPheThrPheSer	171
Qy	568	AGCTTGTGTATGACATCTGGGTCCGCGAGGCTCTAAGGCAAGGGGCTGAGGTGCGAGTT	627
Db	172	SerTyrGlyMetHisTrpValArgGlnAlaProGlyLysGlyLeuGlnTrpValAlaVal	191
Qy	628	ATATCATATGATGAGAGACCTAAATATCTACGAGACTCCGTGAGAGGCGGATTCACCATC	687
Db	192	IleSerTyrAspGlySerAsnLysTyrTyrAlaAspSerValIlyGlyArgPheThrIle	211
Qy	668	TCGAGAGACACTTCCAAAGAACCGGTGATCTTAAAAATGAAACAGCTTGAGACTGAGGAC	747
Db	212	SerArgAspAsnSerLysAsnThrLeuTyrLeuGlnMetAsnSerLeuArgAlaGluAsp	231
Qy	748	ACGGTGTCTATTACTGTGCGGAGAGATCAGAGCTGTGGTGATATGAC-----CAC	801
Db	232	ThrAlaValTyrTyrCysAlaLysAspMetGlyTrpGlySerGlyTyrArgProTyrTyr	251
Qy	802	TACTACGATTGAGACGTCGTGGGGCAAGGGAGACACAGGTACCGTCTCTCAGGATCC	858
Db	252	TyrTyrGlyMetAspValTrpGlyGlnGlyThrThrValThrValSerSerGlyThr	270
RESULT 14			
XX	AAV44995		
XX	ID	AAV44995 standard; protein; 524 AA.	
XX	AC	AAV44995;	
XX	DT	23-MAY-2000 (first entry)	
XX	DE	HD70scFv-Ck-interleukin 2.	
XX	KM	HD70; single-chain Fv fragment; scFv; antibody; 17-1A antigen; human;	
XX	KM	EPCAM; epithelial cell adhesion molecule; inflammatory cytokine; IL-2;	
XX	KM	interleukin-2; Ck-domain; kappa light chain constant domain;	
XX	KM	heteronubind-2; multifunctional compound; immunoglobulin; cytosolic;	
XX	KM	immunostimulatory; anti-leukaemia; diagnosis; prevention;	
XX	KM	antiproliferative; treatment; malignant; haematopoietic cell; lymphoma;	
XX	KM	leukaemia; solid tumour; carcinoma; melanoma; sarcoma.	
OS		Homo sapiens.	
PN		WO200006605-A2.	
XX		10-FEB-2000.	
PD		28-JUL-1999; 99WO-EP005416.	
XX		28-JUL-1998; 98EP-00114082.	
XX		(MIGR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.	
PI		Kufner P, Dreier T, Baenerle PA, Borschert K, Zettl F;	





CC the invention are useful for treating or inhibiting a skeletal dysplasia,  
 CC craniosynostosis or a cell proliferative disorder. The skeletal dysplasia  
 CC is achondroplasia, thanatophoric dysplasia, hypochondroplasia, severe  
 CC achondroplasia with developmental delay or acanthosis nigricans  
 CC dysplasia. The craniosynostosis disorder is Muenke coronal  
 CC craniosynostosis or Crozin syndrome with acanthosis nigricans. The cell  
 CC proliferative disorder is tumour progression that is progression of  
 CC transitional cell carcinoma, osteosarcoma, chondrosarcoma, multiple  
 CC myeloma or mammary carcinoma. This sequence represents the protein  
 CC derived from a Fab expression vector relating to the protein tyrosine  
 CC kinase inhibitor of the invention  
 CC XX

SO Sequence 628 AA;

#### Alignment Scores:

Pred. No.:	1,05e-69	Length:	628
Score:	972.50	Matches:	215
Percent Similarity:	60.854	Conservative:	15
Best Local Similarity:	56.888	Mismatches:	35
Query Match:	56.77%	Indels:	113
DB:	6	Gaps:	5

US-09-194-164-13 (1-918) x ABJ38670 (1-628)

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QY 37 GCACGTGGCTGGTTGGCTACCGTTGGCGAGCCGATATTGTGTGACGAGTCTCCAGGC 96
DB 1 AAlaLeuAlaGlyPheAlaThrValAlaGlnAlaAspIleValLeuThrInserProAla 20
QY 97 ACCGTGCTTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCGAGGGCCAGTCAAGTGT 156
DB 21 ThrLeuSerLeuSerProGlyAlaArgAlaThrLeuSerCysAlaArgAlaSerGlnSerVal 40
QY 157 AGTAGAGCTACTTAGCTGTGATCCAGCAGAAACCTGGCCAGGCTCCAGGCTCTCATC 216
DB 41 SerSerSerTyrLeuAlaThrTyrGlnGlnLysProGlyGlnAlaProArgLeuLeuIle 60
QY 217 TATGTGTGATCCACCGAGGCGCACTGGCAGACAGAGTTTCAGTGGCAGTGGTCCGGG 276
DB 61 TyrGlyAlaSerSerArgAlaThrGlyValProAlaArgPheSerGlySerGly 80
QY 277 ACAGACTTCACCTCCACCATCAGTAGACTGAGACCTGAAGATTGTCAGTATTACTGT 336
DB 81 ThrAspPheThrLeuThrIleSerSerLeuGlnProGlnAspPheAlaValTyrTyrCys 100
QY 337 CAGCAGTATGATGACTCAGCTCAGACACCTCAGATCATTTCGGCGAGGAGCAAGGTG 396
DB 101 GlnGlnHisTyrThrThrPro-----ThrPheGlyGlnGlyThrIlyVal 116
QY 397 GAGATCAACGAACTGGCTGCGTCACCATCTGTC----- 429
DB 117 GluIleLysArgThrValAlaAlaProSerValPheIlePheProProSerAspGlnGln 136
QY 429 ----- 429
DB 137 LeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGlnAla 156
QY 430 -----TCTGGC----- 435
DB 157 LysValGlnTyrLysValAlaAspAlaLeuGlnSerGlyAsnSerGlnGlnSerValThr 176
QY 435 ----- 435
DB 177 GluGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAla 196
QY 436 -----GGTGGCGGTTCCGA 450
DB 197 AspTyrGlnLysHisLysValTyrAlaCysGlnValThrHisGlnGlyLeuSerSerPro 216
QY 451 GGTGTGATCAGTGGAGGTGC----- 474
DB 217 ValThrLysSerPheAsnArgGlyAlaIleMetLysGlnSerThrIleAlaLeuAlaLeu 236
QY 475 -----TCCAGGTGACGCTGGTGAAGTCTGGGGGA 504

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DB 227 LeuProLeuLeuPheThrProValThrIlyAlaGlnValGlnLeuValGlnSerGlyGly 256
QY 505 GCGGTGTCCAGCCCTGGAGAGGTCCCTGAGACTCTCTGTGACGCTCTGAGATTCCCTTC 564
DB 257 GlyLeuValGlnProGlyGlySerLeuArgLeuSerCysAlaAlaSerGlyPheThrPhe 276
QY 555 AGAGCTTGTCTATGACACTGGGTCCGACAGCTCTAGGCAAGGGCTGAGTGGGTGGCA 624
DB 277 SerSerTyrAlaMetSerTyrValArgGlnAlaProGlyLysGlyLeuGlnTyrPValSer 296
QY 625 GTTATATCATATGATGAAGACATAAATACTACGACAGCTCCGTGAAGGGCCGATTCACC 684
DB 297 AlaIleSerGlySerGlyGlySerThrTyrTyrAlaAspSerValLysGlyArgPheThr 316
QY 685 ATCTCCAGAGACACTTCCAGAAACAGGTGATCTTAAATAATGACAGCCTTGAGAACTGAG 744
DB 317 IleSerArgAspAsnSerLysAsnThrLeuTyrLeuGlnMetAsnSerLeuArgAlaGln 336
QY 745 GACAGGCTGTCTATTACTGTGCGCAGAGATCAGAGCCTGTGGGTGACTATGACACACTAC 804
DB 337 AspThrAlaValTyrTyrCysAlaArg-----TyrGlyGlyAspGlyPhe 351
QY 805 TACGGTTTGACGTCTGGGCGAAAGGACCAACGCTCACCGTCTCTCCTCAGATCC 858
DB 352 TyrAlaMetAspTyrTyrPheGlyGlnGlyThrLeuValThrValSerSerAlaSer 369

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Search completed: February 18, 2005, 08:42:17  
 Job time : 106.5 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

## OM nucleic - protein search, using frame\_plus\_nzp model

Run on: February 18, 2005, 08:27:58 ; Search time 22.5 Seconds  
(without alignments)  
6091.364 Million cell updates/sec

Title: US-09-194-164-13

Profile score: 1713

Sequence: 1 GAATTCATGAAAAAACCAGC.....ATCACCATTAGTGAAGCTT 918

## Scoring table:

BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

## Command line parameters:

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-Q=/cgn2\_1/USPRO/epool/US09194164/runat.16022005.122614.6047/app.query.fasta\_1.1095  
-DB=Issued Patents AA -QFMT=fastan -SUFFIX=ra1 -MINMATCH=0.1 -LOOFC=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15  
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-DEV TIMEOUT=130 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

## Database :

Issued Patents AA:\*  
1: /cgn2\_6/pdata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/pdata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/pdata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/pdata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/pdata/1/1aa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/pdata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1573	91.8	304	US-08-862-124-14	Sequence 14, Appl
2	1451.5	84.7	287	US-08-862-124-17	Sequence 17, Appl
3	928	54.2	352	US-09-203-958A-2	Sequence 2, Appl
4	926.5	54.1	456	US-09-495-880A-11	Sequence 11, Appl
5	892	52.1	283	US-09-420-592A-6	Sequence 6, Appl
6	892	52.1	283	US-09-985-442-6	Sequence 6, Appl
7	892	52.1	283	US-09-983-580-6	Sequence 6, Appl
8	887	51.8	263	US-09-069-821-3	Sequence 3, Appl
9	887	51.8	263	US-09-956-086-3	Sequence 3, Appl
10	887	51.8	263	US-09-956-087-3	Sequence 3, Appl
11	865	50.5	354	US-09-393-627B-28	Sequence 28, Appl
12	827.5	48.3	240	US-08-488-113B-147	Sequence 147, App

13	827.5	48.3	240	US-08-477-484B-147	Sequence 147, App
14	827.5	48.3	240	US-08-646-360-147	Sequence 147, App
15	827.5	48.3	240	US-08-839-765-147	Sequence 147, App
16	827.5	48.3	240	US-09-136-389-147	Sequence 147, App
17	827.5	48.3	240	US-09-610-838-147	Sequence 147, App
18	827.5	48.3	240	US-09-711-485-147	Sequence 147, App
19	808.5	47.2	409	US-09-554-765-14	Sequence 14, Appl
20	805	47.0	408	US-09-554-765-15	Sequence 15, Appl
21	784	45.8	271	US-08-400-115-4	Sequence 4, Appl
22	784	45.8	374	US-09-646-028-15	Sequence 15, Appl
23	779.5	45.5	491	US-10-011-125A-2	Sequence 2, Appl
24	777	45.4	599	US-08-442-542-18	Sequence 18, Appl
25	777	45.4	599	US-08-765-469-18	Sequence 18, Appl
26	766	44.7	298	US-09-318-661-2	Sequence 2, Appl
27	766	44.7	298	US-09-883-758-2	Sequence 2, Appl
28	756	44.1	244	US-08-392-338A-13	Sequence 13, Appl
29	756	44.1	244	US-09-166-750-13	Sequence 13, Appl
30	756	44.1	244	US-09-166-093-13	Sequence 13, Appl
31	756	44.1	244	US-09-172-019-13	Sequence 13, Appl
32	756	44.1	244	US-09-166-094-13	Sequence 13, Appl
33	756	44.1	244	US-09-443-213-13	Sequence 13, Appl
34	755	44.1	239	US-08-860-174A-2	Sequence 2, Appl
35	744	43.4	242	US-08-224-591-14	Sequence 14, Appl
36	744	43.4	242	US-08-392-338A-23	Sequence 23, Appl
37	744	43.4	242	US-08-926-789-14	Sequence 14, Appl
38	744	43.4	242	US-09-166-750-23	Sequence 23, Appl
39	744	43.4	242	US-09-166-093-23	Sequence 23, Appl
40	744	43.4	242	US-09-172-019-23	Sequence 23, Appl
41	744	43.4	242	US-09-166-094-23	Sequence 23, Appl
42	744	43.4	242	US-09-443-213-23	Sequence 23, Appl
43	744	43.4	244	PCT-US93-11138-14	Sequence 14, Appl
44	744	43.4	285	US-09-318-661-4	Sequence 4, Appl
45	744	43.4	285	US-09-883-758-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-08-862-124-14

; Sequence 14, Application US/08862124

; Patent No. 6207153

GENERAL INFORMATION:

APPLICANT: Dan, Michael D.

APPLICANT: Maiti, Prady K.

TITLE OF INVENTION: KAPLAN, Howard A.

TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE

TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND DETECTION OF CANCERS

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Morrieon & Foerster LLP

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/862,124

FILING DATE: 22-MAY-1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Lehnardt, Susan K.

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 31608-20001.20

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 813-5600

TELEFAX: (650) 494-0792

TELEX: 706141  
 INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 304 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-862-124-14

## Alignment Scores:

Pred. No.:	3e-124	Length:	304
Score:	1573.00	Matches:	302
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	91.83%	Indels:	0
DB:	3	Gaps:	0

US-09-194-164-13 (1-918) x US-08-862-124-14 (1-304)

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QY 1 GAATTGATGAAAAAACCCTATCGGATCGAGTTGCGACTGGCTGTTCCGTACCGTT 60
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DB 1 GluphemeLysThrAlaIleAlaIleAlaValAlaLeuAlaGlyPheAlaThrVal 20

QY 61 GGGCAGCCGATATTGTTGACGAGTCTCCAGGACCGCTTGTCTTCACGGGAAA 120
    |||
DB 21 AlaGlnAlaAspIleValLeuThrGlnSerProGlyThrLeuSerLeuSerProGlyGln 40

QY 121 AGAGCCACCTCTCTCTGAGGCGGAGTCAAGTGTATAGCAGCTACTTACCTGGTAC 180
    |||
DB 41 ArgAlaThrLeuSerCysArgAlaSerGlnSerValSerSerSerYrLeuAlaTrpYr 60

QY 181 CAGCAGAAACCTGGCCAGGCTCCAGGCTCTCATCTATGTTGCATCCACGAGGCACT 240
    |||
DB 61 GlnGlnLysProGlyGlnAlaProArgLeuLeuIleTyrGlyAlaSerThrArgAlaThr 80

QY 241 GGCATGCCAGACAGTTGAGTGGAGTGGGTCGGGAGACGTTCACTCTCCACCATCAGT 300
    |||
DB 81 GlyMetProAspArgPheSerSerGlySerGlyThrAspPheThrLeuThrIleSer 100

QY 301 AGACTGAGACCTGAAAGATTGTCAGTGTATTACTGTCAAGCATGATGATGACCTCAG 360
    |||
DB 101 ArgLeuGlnProGlnPheAlaValTyrTyrCysGlnGlnIleTyrGlySerSerProGln 120

QY 361 ACACTTCAGATCACTTTCCGCGAGGAGACCAAGTGAAGATCAAAGAACTGTGGTGA 420
    |||
DB 121 ThrProGlnIleThrPheGlyGlyGlyThrLysValGlnIleLysArgThrValAlaAla 140

QY 421 CCATCTGTCTGGCGGCGGCGGTTCCGAGGAGTGGATCAAGTGAAGTGGCTCCAG 480
    |||
DB 141 ProSerValSerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyGln 160

QY 481 GTGCAGCTGGTGAAGTCTGGGGAGGCGTGTTCAGCTCGGAGAGTCCCTGAGACTCTCC 540
    |||
DB 161 ValGlnLeuValGlnSerGlyGlyGlyValGlnProGlyArgSerLeuArgLeuSer 180

QY 541 TGTGCAGCTCTGGATTTCCCTTCAAGACTTGTGATGCACTGGGTCGCCAGGCTCTA 600
    |||
DB 181 CysAlaAlaSerGlyPheProPheArgSerPheAlaMetHisTrpValArgGlnAlaLeu 200

QY 601 GGCAGAGGGCTGAGTGGGAGTGGGAGTATATCATATGATGAAGCACTAAATACACGA 660
    |||
DB 201 GlyLysGlyLeuGlnIleValAlaValIleSerTyrAspGlySerThrIleTyrTrpAla 220

QY 661 GACTCCGTGAAGGCGCATTCACCATCTCCAGAGCACTTCCAGAAACGCTGATCTTA 720
    |||
DB 221 AspSerValLysGlyArgPheThrIleSerArgAspThrSerIleAsnThrValTyrLeu 240

QY 721 AAAATGAACGCTGGAACCTGAGGACAGGCTGTCTATTAATCTGTGCGAGATCAGAGC 780
    |||
DB 241 LysMetAsnSerLeuArgThrGlnAspThrAlaValTyrTyrCysAlaArgAspGlnSer 260

QY 781 CGTTGGGAGCATATGACCACTACGCTTGGAGTGGGCGGAGGAGCAAGGCGCAGGCGC 840
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DB 261 LeuLeuGlyAspTyrAspHisTyrTyrGlyLeuAspValTrpGlyLysGlyThrThrVal 280

QY 841 ACCGTTCTCTGAGATCCGAACAAAACCTGATCAGCGAAGAGATCTGACCATACCAT 900
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DB 281 ThrValSerSerGlySerGlnGlnIleLeuIleSerGlnGlnIleAspLeuAsnHisHis 300

QY 901 CACCAT 906
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DB 301 HisHis 302

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## RESULT 2

US-08-862-124-17  
 Sequence 17, Application US/08862124  
 Patent No. 6207153

## GENERAL INFORMATION:

APPLICANT: Dan, Michael D.  
 APPLICANT: Maili, Pradi K.  
 TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND  
 NUMBER OF SEQUENCES: 28  
 CORRESPONDENCE ADDRESS:  
 ADDRESSER: Morrison & Foerster LLP  
 STREET: 755 Page Mill Road  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94304-1018

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/862,124  
 FILING DATE: 22-MAY-1997  
 CLASSIFICATION: 424

## ATTORNEY/AGENT INFORMATION:

NAME: Lehnardt, Susan K.  
 REGISTRATION NUMBER: 33,943  
 REFERENCE/DOCKET NUMBER: 31608-20001.20  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650) 813-5600  
 TELEFAX: (650) 494-0792

## INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 287 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-862-124-17

## Alignment Scores:

Pred. No.:	4.91e-114	Length:	287
Score:	1451.50	Matches:	283
Percent Similarity:	93.71%	Conservative:	0
Best Local Similarity:	93.71%	Mismatches:	2
Query Match:	84.73%	Indels:	17
DB:	3	Gaps:	1

US-09-194-164-13 (1-918) x US-08-862-124-17 (1-287)

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    |||
DB 1 GluphemeLysThrAlaIleAlaIleAlaValAlaLeuAlaGlyPheAlaThrVal 20

QY 61 GGCAGCCGATATTGTTGACGAGTCTCCAGGACCGCTTGTCTTCACGGGAAA 120
    |||
DB 21 AlaGlnAlaAspIleValLeuThrGlnSerProGlyThrLeuSerLeuSerProGlyGln 40

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QY	181	CAGCAGAAACCTTGCCAGGAGCTCCACAGCTTCATATAGTGCATCCACAGGGCCACT	240	
Db	61	GLINGLINYPROGLYGLINLAPROARGLEULENILETYRGLYLAASERTHARGALATHR	80	
QY	241	GGCATGCCAGACAGGTTCAGTGGCAGTGGGTCCGGGACAGACTTCACCTCCACCATAGT	300	
Db	81	GLYMETPROASPARGPHEISERGLYSERGLYTHRASPHERHTHLEUTHRIILESER	100	
QY	301	AGACTGGAGCCCGTAGATTTTGAGAGTGTTACTGTGCAGAGATAGTGAGTCAACCTCAG	360	
Db	101	ARGLEUGLUPROGLINASPHEALVALTYTRYCYSGINGLINTRYGLYSERSEPROGLIN	120	
QY	361	ACACCTCAGATCACTTTCGCGGAGGAGACCAAGAGTGAAGATCAACGAACCTTGAGCTGCA	420	
Db	121	THRPROGLINILETHRPHEDLYGLYGLYTHIRLYSVALGLINILEYARGHTRVALALALAL	140	
QY	421	CCATCTGTCTCTGGCGGTGCGGATTCGGAGGTGTGATCAGGTGAGGTGGCTCCAG	480	
Db	141	-----SERGLYGLIN	143	
QY	481	GTGCAGCTGTGTGAGTCTTGGGGGAGGCGGTGTCCACCTCGGAGGTCCCTGGAACCTCTCC	540	
Db	144	VALGINLEUVALGLINSEIRGLYGLYGLYVALVALGINPROGLYARGSERLEUARGLEUSER	163	
QY	541	TGTGCAGCGCTTGAGATTCCCTTCAGAACTTGTCTATGACACTGGGTCGCGCAGGCTCTA	600	
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QY	601	GGCAAGGGGCTGTGAGTGGGTGGCACTGTATATCATATGATGAGACACTAAATCTACGCA	660	
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QY	661	GACTCCGTGGAAGGGCGGATTCACCATCTCCAGAGACACTTCCAAAGACACGGTGTATCTA	720	
Db	204	ASPSEIRVALYVGLYARGPHERHTRIILESEARGASPTHRSEIRLYSASANTHRVALITYRLEU	223	
QY	721	AAAAAGAACAGGCTGTGAACTGAGGACAGAGGCGTGTATTACTGTGCGAGAGATCAAGAC	780	
Db	224	LYSMECHANSEIRLEUARGTHRGLINSPHTRALVALITYTRYCSALARGARGLINSEIR	243	
QY	781	CTGTTGGGTGACTATATGACCACTACTACGGTTTGACAGCTGGGGGCAAGGAGCACGAGTC	840	
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QY	841	ACCGTCTCTCTCAGATTCGGAACAAAACCTGATCAGGGAAGAAGATGAAACCATCAACAT	900	
Db	264	THRVALISERSERGLYSERGLINGLYLEULILESERGLUGLUNAPREUENHSHIHSHIS	283	
QY	901	CACCAT 906		
Db	284	HHSHS 285		
RESULT 3				
US-09-203-958A-2				
Sequence 2, Application US/09203958A				
Patent No. 6682928				
GENERAL INFORMATION:				
APPLICANT: KELER, Tibor				
APPLICANT: GOLDSTEIN, Joel				
APPLICANT: GRAZIANO, Robert				
APPLICANT: DEO, Yashwant M.				
TITLE OF INVENTION: CELLS EXPRESSING ANTI-FC RECEPTOR				
TITLE OF INVENTION: BINDING COMPONENTS				
FILE REFERENCE: MXI-099CPA				
CURRENT APPLICATION NUMBER: US/09/203, 958A				
CURRENT FILING DATE: 1998-12-02				
PRIOR APPLICATION NUMBER: 60/067232				
PRIOR FILING DATE: 1997-12-02				
NUMBER OF SEQ ID NOS: 4				

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1  SOFTWARE: FastSeq for Windows Version 4.0
2  ; SEQ ID NO: 2
3  ; LENGTH: 352
4  ; TYPE: PRF
5  ; ORGANISM: Artificial Sequence
6  ; FEATURE:
7  ; OTHER INFORMATION: Synthetic construct
8  US-09-203-958A-2
9
10 Alignment Scores:
11 Pred. No.: 5,65e-70 Length: 352
12 Score: 928.00 Matches: 192
13 Percent Similarity: 75.43% Conservative: 26
14 Best Local Similarity: 66.44% Mismatches: 45
15 Query Match: 54.17% Indels: 26
16 DB: 4 Gaps: 5
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18 US-09-194-164-13 (1-918) x US-09-203-958A-2 (1-352)
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20 QY 52 GCTACCGCTTGGCCGACGGCCGATATTGTGTAGCAGACTTCCAGGACCGCTGCTTGTCT 111
21 Db 32 AAGAGnProAlaArgSerAspIleGlnLeuThrGlnSerProSerLeuSerAlaSer 51
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23 QY 112 CCAGGGGAAAGGCCACCTCTCCCTGCAGGGCCACGACAGTCTT----- 155
24 Db 52 ValGlyAspAlaArgValThrIleThrCysLysSerSerGlnSerValLeuTyrSerSerAsn 71
25
26 QY 157 AGTAGCAGCTACTTTCAGCTGTATACAGGCGAAACCTGGCCAGGCTCCAGGCTCCTCATC 216
27 Db 72 GlnLysAsnTyrLeuAlaTrrPyrGlnGlnLysProGlyValAlaTrrPylSerLeuLeuIle 91
28
29 QY 217 TATGGTGCATCCACGAGGGCCACTGGCATGCCAGACAGATTCAGTGGAGTGGTCCGG 276
30 Db 92 TrrTrrPylAsnSerThrArgGlnSerGlyValProSerArgPheSerGlySerGly 111
31
32 QY 277 ACAAGCTTCACCTCAACCATCACTAGACTGAGAGCTGAAAGATTTCAGCTGTATTACTGT 336
33 Db 112 ThrAspPheThrPheThrIleSerSerLeuGlnProGlnAspIleAlaThrTrrTrrCys 131
34
35 QY 337 CAGCAGTATGATGGATCCACCTCAGACACTCAGATCACTTTCGGCGGAGGACCAAGGTG 396
36 Db 132 HisGlnTrrLysSerSer-----TrrPheGlnGlnGlnTrrLysVal 146
37
38 QY 397 GAGATCAACACGAACTGTGGCTGACCACTGCTGCTGGCGGTGGCCGTTCCGAGGTGCT 456
39 Db 147 GlnIleLysSer-----SerGlyGlyGlySerGlyGlyGly 155
40
41 QY 457 GGATCAGGTGAGAGTGGCTCCAGGTGCAGCTGTGGAGACTTGGGGGAGGCGGTGTCAG 516
42 Db 160 GlySerGlyGlyGlyGlySerGlnValGlnLeuValGlnSerGlyGlyGlyValGln 179
43
44 QY 517 CCTGGGAGAGTCCCTGAGACTCTCCCTGTGGAGGCTCTGATTCCTCCCTCAGAAAGCTTTC 576
45 Db 180 ProGlnAspSerLeuArgLysSerCysSerSerSerGlyPheIlePheSerAsnTyr 199
46
47 QY 577 ATGCAGCTGGTCCGCGCAGGCTCTTACGACAAAGGGGCTGAGATGGGTGCAGTTATATCATAT 636
48 Db 200 MetTrrTrrPylValArgGlnAlaProGlyLysGlyLeuGlnTrrPylAlaThrIleSerAsp 219
49
50 QY 637 GATGGAACACTAAATACTACGACAGACTCCGTGAAGGGCGATTCCACATCTCCAGAGAC 696
51 Db 220 GlyGlySerTrrTrrTrrTrrProAspSerValLysGlyArgPheThrIleSerArgAsp 239
52
53 QY 697 ACTTCCAGAAACACGGGTATTTAAATAAGAACACGCTGAGAAACTGAGACACAGCGCTGC 756
54 Db 240 AsnSerLysAsnTrrLysLeuPheLeuGlnMetAspSerLeuArgProGlnAspTrrGlyVal 259
55
56 QY 757 TATTACTGTGCGAGAGATCAGAGCTGTTGGGTGACTATGACACACTACACGATTTGGAC 816
57 Db 260 TrrPheCysAlaArg-----GlyTrrTrrArgTrrGlyGlnLysAlaMetAsp 274
58
59 QY 817 GTCGTGGGCAAGAAGGACCGGTCCCGTCTCTCAGAGA-----TCCGAACA 864
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Db      275 TyrTpglynglnGlyThrProValThrValSerSerProArgLeuGlnValAspGluGln 294
QY      865 AAAGTATGACGGAAGAGATCTGAAC 891
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Db      295 LysLeuIleSerGluGlnAspLeuAsn 303
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RESULT 4
US-09-495-880A-11
; Sequence 11, Application US/09495880A
; Patent No. 6667150
; GENERAL INFORMATION:
; APPLICANT: RUDERT, FRITZ
; APPLICANT: GE LIMITING
; APPLICANT: ILAG, VIC
; TITLE OF INVENTION: NOVEL METHOD AND PHAGE FOR THE IDENTIFICATION OF
; TITLE OF INVENTION: NOCLEIC ACID SEQUENCES ENCODING MEMBERS OF A MULTIMERIC
; FILE REFERENCE: MORPHO/9
; CURRENT APPLICATION NUMBER: US/09/495,880A
; CURRENT FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: PCT/EP98/04836
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: EP 97 11 3319.4
; PRIOR FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 456
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ompA-flag-scfv (anti-
; OTHER INFORMATION: HA6)-gene IIIs encoded by phage vector fhagla (circular)
US-09-495-880A-11

Alignment Scores:
Pred. No.:      8, 08e-70      Length:      456
Score:          926.50        Matches:      130
Percent Similarity: 75.42%    Conservative: 37
Best Local Similarity: 63.12% Mismatch:      49
Query Match:    54.09%       Indels:       25
DB:              4           Gaps:          6

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        |||
QY      67 GCC-----GATTGCTGTGACGCGAGTCCGAGGACCCCTGCTTGTGCTCCAGG 117
        |||
Db      21 AlaAspTyrLysAspIleValMetIleGlnSerProSerSerLeuThrValThrAlaGly 40
        |||
QY      118 GAAAGAGCCACCTCTCTCGACGAGCGAGTTCAGAGTGTAGTACAGC----- 165
        |||
Db      41 GluLysValThrMetSerCysThrSerSerGlnSerLeuPheAsnSerGlyLysGlnLys 60
        |||
QY      166 ---TACTTACCTGCTGACGAGCAAGAAACCTGCGCAGGCTCCAGGCTCCTCATCTATG 222
        |||
Db      61 AsnTyrLeuThrTyrPyrGlnGlnLysProGlyGlnProGlySerValLeuIleTyrTrp 80
        |||
QY      223 GCAATCACAGGCGCCACCTGCGATGCGACAGTTCAGTTCAGGAGCGGTCCGGGACAGAC 282
        |||
Db      81 AlaSerThrArgLysGlnSerGlyValProAspArgPheThrIleLysSerGlySerGlyTrpAsp 100
        |||
QY      283 TTCACCTCAGCAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGT 342
        |||
Db      101 PheThrLeuThrIleSerSerValGlnAlaGlnAspLeuAlaValTyrTyrCysGlnAsn 120
        |||
QY      343 TATGTAGTACCTCAGTACAGACACTCAGATCATTTCGGCGGAGGAGCAAGGTGAGATC 402
        |||
Db      121 AspTyrSerAsnPro-----LeuThrPheGlyGlyGlyThrIleLysLeuGlnLeu 136

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QY      403 AAAGAACTGAGGCTGACCACTCT-----GTCTTGCGCGT 438
        |||
Db      137 LysArgAlaGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlySerGlyGly 156
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QY      439 GCGCGTTCCGAGGTGTGATGATCAGGTGAGGTGAGTCTCCAGGTGACGTGAGTCT 498
        |||
Db      157 GlyIleSerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGly 176
        |||
QY      499 GGGGAGCGGTGCTCCAGCTGCGGAGGCTCCTGAGACTCTCTGTCGAGCGCTGAGATTC 558
        |||
Db      177 GlyIleAspLeuValLysProGlyLysSerLeuLysSerCysAlaIleSerGlyPhe 196
        |||
QY      559 CCTTCAGAGCTTGTGCTATGCTACACTGAGTCCGCGCAGCTTACAGGAGGCGGTGAGTGG 618
        |||
Db      197 SerPheSerSerTyrGlyMetSerTyrValArgIleThrProAspLysArgLeuIleTrp 216
        |||
QY      619 GTGGCAGTTATATCATATGATGAGAAACACTAAATCTACGACAGACTCCGTGAAGGCCGA 678
        |||
Db      217 ValAlaThrIleSerAsnGlyGlyGlyTyrThrTyrTyrProAspSerValLysGlyArg 236
        |||
QY      679 TTCACCATCTCCAGAGACACTTCCAGAAACGCGGTATCTAAATGAAACAGCTGAGA 738
        |||
Db      237 PheThrIleSerArgAspAsnAlaLysAsnThrLeuTyrLeuGlnMetSerSerLeuLys 256
        |||
QY      739 ACTGAGACACAGGCTGTCTATTACTGTGTCGAGAGATCAGAGCTGTTGGTACTATGAC 798
        |||
Db      257 SerGluAspSerAlaMetTyrTyrCysAlaIleArgGluArg-----TyrAsp 272
        |||
QY      799 CACTACTACGCTTGTGAGCGTCTGGGCGCAAGGAGCACGCTGACCGTCTCTCAGAGATCC 858
        |||
Db      273 Glu---AsnGlyPheAlaTyrTrpGlyGlnGlyThrLeuValThrValSerAlaSerGly 291
        |||
QY      859 GAA 861
        |||
Db      292 Glu 292

RESULT 5
US-09-420-592A-6
; Sequence 6, Application US/09420592A
; Patent No. 6333396
; GENERAL INFORMATION:
; APPLICANT: Filpula, David R.
; APPLICANT: Wang, Maoliang
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: No. 6333396el Method for Targeted Delivery of Nucleic Acids
; FILE REFERENCE: 0977.2300001
; CURRENT APPLICATION NUMBER: US/09/420,592A
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/104,949
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 283
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Kabat
; OTHER INFORMATION: Consensus
; NAME/KEY: UNSURE
; LOCATION: (232)
; OTHER INFORMATION: May be any amino acid.
; NAME/KEY: UNSURE
; LOCATION: (234)
; OTHER INFORMATION: May be any amino acid.
; NAME/KEY: UNSURE
; LOCATION: (239)
; OTHER INFORMATION: May be any amino acid.
US-09-420-592A-6

Alignment Scores:
Pred. No.:      5, 71e-67      Length:      283
Score:          892.00        Matches:      181

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DB 172 LysGlyLeuGluTrpValSerValIleSerGlyLysThrAspGlyLysSerThrTrpTrp 191  
QY 658 GCAAGACTCCGTGAAGGGCGGATTACCATCTCCAGAGACATTCCAAAGACCGGTAT 717  
DB 192 AlaAspSerValIleGlyPheThrIleSerArgAspAsnSerLysAsnThrLeuTrp 211  
QY 718 CTAATAATGAACAGCTTGAGACTGAGACAGCGCTGTATTACTGTGCGAGATGAG 777  
DB 212 LeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTrpCysAlaArgGlyArg 231  
QY 778 -----AGCTGTGGGTGACTATGACCACTACTACGCTTGGAGCGTGGGCAAA 828  
DB 232 \*\*\*Gly\*\*\*SerLeuSerGly\*\*\*TyrTrpTrpTrpTrpTrpTrpTrpTrpTrp 251  
QY 829 GGGACCAAGGTCAACGCTCTCTCAGAGATCCGAACAAA 867  
DB 252 GlyThrLeuValThrValSerSerLysLysLysLysLys 264  
RESULT 7  
US-09-983-580-6  
Sequence 6, Application US/09983580  
Patent No. 6764853  
GENERAL INFORMATION:  
APPLICANT: Filipula, David R.  
APPLICANT: Wang, Maoliang  
APPLICANT: Whitlow, Marc D.  
TITLE OF INVENTION: No. 6764853el Method for Targeted Delivery of Nucleic Acids  
FILE REFERENCE: 0977.2300002  
CURRENT APPLICATION NUMBER: US/09/983,580  
PRIORITY FILING DATE: 2001-10-25  
PRIORITY FILING DATE: 1999-10-19  
PRIORITY FILING DATE: 1998-10-20  
PRIORITY FILING DATE: 1998-10-20  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 283  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Kabat  
OTHER INFORMATION: Consensus  
NAME/KEY: UNSURE  
LOCATION: (232)  
OTHER INFORMATION: May be any amino acid.  
NAME/KEY: UNSURE  
LOCATION: (234)  
OTHER INFORMATION: May be any amino acid.  
NAME/KEY: UNSURE  
LOCATION: (239)  
OTHER INFORMATION: May be any amino acid.  
US-09-983-580-6  
Alignment Scores:  
Pred. No.: 5.71e-67 Length: 283  
Score: 892.00 Matches: 181  
Percent Similarity: 76.92% Conservative: 29  
Best Local Similarity: 66.30% Mismatches: 47  
Query Match: 52.07% Indels: 16  
DB: 4 Gaps: 5  
US-09-194-164-13 (1-918) x US-09-983-580-6 (1-283)  
QY 70 GATATTGTGTGACGAGCTCAGGACCCCTGCTTGTCTCCAGGAGAAAGACACC 129  
DB 1 AspIleGlnMetThrValSerProSerSerLeuSerAlaSerValAlaPheGlyValThr 20  
QY 130 CTCCTCGAGAGGCGAGTCAAGTGT-----AGTAGAGACTACTTACGCTGTAACAG 183  
DB 21 IleThrCysArgAlaSerGlnSerLeuValSerIleSerAsnTrpLeuAlaTrpGln 40

QY 184 CAGAACCTGGCAGAGCTCCAGGCTCCTCATCTATGCTGATCCAGCAGGCGCATGAC 243  
DB 41 GlnLysProGlyLysAlaProLysLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGly 60  
QY 244 ATGCCAGACAGTTTCAGTGGCAGTGGCTCCGAGACAGACTTCACTTCACTCAGTGA 303  
DB 61 ValProSerArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSer 80  
QY 304 CTGAGACCTGAAGATTTTGGACGTGATTAAGTGCAGAGTATGATGCTCACTCAGACA 363  
DB 81 LeuGlnProGluAspPheAlaThrTrpTrpCysGlnGlnTrpAsnSer-----Leu 97  
QY 364 CCTCAGATCACTTTGGCGAGAGGACCAAGGTGAGATCAACGACTGTGGCTGACACA 423  
DB 98 ProGluTrpThrPheGlyGlnGlyThrLysValGluIleLysGlySer----- 113  
QY 424 TCTGTCTGTGGCGGTGGCGGTTCGAGAGGTGGATCAGGTGAGGTGCTCCAGGTG 483  
DB 114 -----ThrSerGlySerGlyLysProGlySerGlyGlnGlySerThrLysGlyLysVal 131  
QY 484 CAGCTGTGAGATCTGGGAGAGCGCTGATCCAGCTCGGAGAGGTCCCTGAGACTCTCTGT 543  
DB 132 GlnLeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeuSerCys 151  
QY 544 GCAAGCTGTGATCCCTTCAAGACTTGTGATGACTGGGTCCGCGAGGCTCTAGGC 603  
DB 152 AlaAlaSerGlyPheThrPheSerSerTyrAlaMetSerTrpValArgGlnAlaProGly 171  
QY 604 AAGGGCTGAGTGGGTGGCAGTTATATCA-----TATGATGAGACATTAATATCTAC 657  
DB 172 LysGlyLeuGluTrpValSerValIleSerGlyLysThrAspGlyGlySerThrTrpTrp 191  
QY 658 GCAAGCTCCGTGAAGGGCGGATTCACCATTCACAGACACTTCCAAAGACAGGATAT 717  
DB 192 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTrp 211  
QY 718 CTAATAATGAACAGCTTGAGACTGAGACAGCGCTGTATTACTGTGCGAGATGAG 777  
DB 212 LeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTrpTrpCysAlaArgGlyArg 231  
QY 778 -----AGCTGTGGGTGACTATGACCACTACTACGCTTGGAGCGTGGGCAAA 828  
DB 232 \*\*\*Gly\*\*\*SerLeuSerGly\*\*\*TyrTrpTrpTrpTrpTrpTrpTrpTrpTrp 251  
QY 829 GGGACCAAGGTCAACGCTCTCTCAGAGATCCGAACAAA 867  
DB 252 GlyThrLeuValThrValSerSerLysLysLysLysLys 264  
RESULT 8  
US-09-069-821-3  
Sequence 3, Application US/09069821  
Patent No. 6323322  
GENERAL INFORMATION:  
APPLICANT: FILIPULA, DAVID  
APPLICANT: WANG, MAOLIANG  
APPLICANT: SHORR, ROBERT  
APPLICANT: WHITLOW, MARC  
APPLICANT: LEE, LISHYNG S.  
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVE., NW, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30









Sequence 147, Application US/08488113B  
Patent No. 574380  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studinka, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,113B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-9155  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ. ID NO: 147:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-488-113B-147  
Alignment Scores:  
Pred. No.: 1,466-61 Length: 240  
Score: 827.50 Matches: 161  
Percent Similarity: 75.86 Conservative: 37  
Best Local Similarity: 61.69 Mismatches: 42  
Query Match: 48.31 Indels: 21  
DB: 1 Gaps: 5  
US-09-194-164-13 (1-918) x US-08-488-113B-147 (1-240)  
QY 70 GATATTGTCGACGAGTCTCCAGGACCCCTTTTCCTCCAGGGAGAGCCACC 129  
DB 1 AspIleGlnMetThrIleSerProSerLeuSerValGlyAspArgValThr 20  
QY 130 CTCCTCGAGGCGGACGACGAGTGTAGTAGCAGCTACTAGCTGATACAGAGAA 189  
DB 21 ILeThrCysArgIleSerGlnAspIle---AenSerTyrLeuSerTrpPheGlnGlnLys 39

QY 190 CTTGGCCAGGCTCCAGGCTCCTCATCTATGATGATCCACAGGCGCATGGATGCCA 249  
DB 40 ProGlyLysAlaProLysThrLeuLerTyrArgAlaMetArgLeuSerValPro 59  
QY 250 GACAGTTCAGTGGCAGTGGTCCGGACAGACTTCACTTCACCATCAGTAGAG 309  
DB 60 SerArgPheSerGlySerGlySerGlyThrAspTyrThrLeuThrIleSerSerLeuGln 79  
QY 310 CTTGAAGATTTTGCAGTGTATTACTGTACGACAGTATGAGTACTACCTCAGACCTCAG 369  
DB 80 TyrGlnAspPheGlyIleTyrTyrCysGlnGlnTyrAspGluSerProTyr----- 96  
QY 370 ATCACTTGGGGGAGGAGCCAGGTGGAGATCAACAGCACTGTGGCTGACCATCTGTC 429  
DB 97 ---ThrPheGlyGlyGlyThrLysLeuGlnLys----- 107  
QY 430 TCTGGCGGTGGCGGTTCGAGAGTGTGATCAGGTGAGGTGCTCCAGGTGACGTG 489  
DB 108 ---GlyGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyGlyGlyGly 126  
QY 490 GTGAGTCTGGGGGAGCGGTGTGCTCAGGAGGTCTGAGACTCTCTGTGACGCC 549  
DB 127 ValGlnSerGlyGlyGlyLeuValLysProGlyLysSerValArgIleSerCysAlaIle 146  
QY 550 TCTGATTCCTCCCTCAGAAAGCTTGTGCTATGCACTGAGGTGGCGGAGGTCTGAGCAAGGG 609  
DB 147 SerGlyTyrThrPheThrAsnTyrGlyMetAsnTrpValArgGlnAlaProGlyLysGly 166  
QY 610 CTGAGGTGGTGGCAGTTATATCATATGATGAGAACATAATACAGCACTCCGTG 669  
DB 167 LeuGluTrpMetGlyTyrPheAsnThrHisThrGlyGluProThrTyrAlaAspSerPhe 186  
QY 670 AAGGCCCATTCACCATCTCCAGAGACCTTCCAAAGAACAGGCTATCTAAATGAC 729  
DB 187 LysGlyArgPheThrPheSerLeuAspAspSerLysAsnThrAlaTyrLeuGlnIleAsn 206  
QY 730 AGCCTGAGACATCGAGGACGAGCGTGTATTACTGTGCGAGATCAAGGCTGTGGGT 789  
DB 207 SerLeuAlaGlnAlaAspThrAlaValTyrPheCysThrArg-----Arg 221  
QY 790 GACTATGACCACTACTACGAGTTTGGACGCTCTGGGGCAAGGAGCACCGGTCTCC 849  
DB 222 GlyTyrAspTyrPyrPhe-----AspValTrpGlyGlnGlyThrThrValThrValSer 239  
QY 850 TCA 852  
DB 240 Ser 240  
RESULT 13  
US-08-477-484B-147  
Sequence 147, Application US/08477484B  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studinka, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:



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TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/707-8889
/ TELEFAX: 312/707-9155
/ TELEX: 650 388-1248
/ INFORMATION FOR SEQ ID NO: 147:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 240 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-646-360-147

Alignment Scores:
Pred. No.: 1,46e-61 Length: 240
Score: 827.50 Matches: 161
Percent Similarity: 75.86% Conservative: 37
Best Local Similarity: 61.69% Mismatches: 42
Query Match: 48.31% Indels: 21
DB: 2 Gaps: 5

US-09-194-164-13 (1-918) x US-08-646-360-147 (1-240)
QY 70 GATATTGTGTGACGACGCTCCAGGACCTGTTGTCAGGGGAAAGACCACC 129
Db 1 AspIleGIeImetThrgInSerProSerSerleuSerAlaSerValGIaSpArgValThr 20
QY 130 CTGTCCTGGAGGGCGACGTGAGTGTAGAGAGCTACTTACCTGTGATACCGAGAAA 189
Db 21 ILehThcYsaIrGaIaSerGIaSepIle--AsnSerIreIuSerIrPpneGIaInIlyS 39
QY 190 CTTGGCCAGGCTCCAGGCTCTCATCTATGTGATGATCCAGGCGCACCTGGCATGCCA 249
Db 40 ProGIlySaIaIaProIySthreIuIleIyIrArGIaIaSaIrGleuGIuSerGIyValPro 59
QY 250 GACAGGTTCAGTGTGACGTGGTCCGGACAGACTTCACTTCCATCAGTACGTGAG 309
Db 60 SerArGheserGIySerGIySerGIyThraSpIyThreIuThrlIeSerSerleuGIaIn 79
QY 310 CCTGAAGATTGTCAGTGTATTAAGTGTGACAGTATGTAGTACCTGACCTGACACTGAG 369
Db 80 TyrGIaIaSpheGIyIleIyTrYrCYaGIaInIlyrAspGIuSerProIrP----- 96
QY 370 ATCACTTTCGGCGGAGGACCAAGGTGAGATCAAAAGACTGTGCTGCACCATCTGTC 429
Db 97 ---ThrPheGIyGIyGIyThrlYrIeGIuIleGIy----- 107
QY 430 TCTGGGGGTGGCGGTTCGGAGGTGTGATCAGGTGAGAGTGGCTCCAGGTGACGCTG 489
Db 108 ---GIyGIyGIyGIySerGIyGIyGIySerGIyGIyGIySerGIyGIySerGIyIleGIuInleu 126
QY 490 GTGAGATCTGGGGGAGCGGTGTCCAGGCTGGGAGGTCCCTGAGACTCTCTGTGACGCC 549
Db 127 ValGIaInSerGIyGIyGIyIleuValIySProGIyGIySerValArGIaIeSerCYaIaIa 146
QY 550 TCTGAATTCCTCTTCAAGACCTTGTATGACACTGTGGGTCCGCGAGGCTCTAGGCAAGGG 609
Db 147 SerGIyTrYrThrPheThraSenIyIrGIyMeIaSnIrPValArGIaInIaIaProGIyIyGIy 166
QY 610 CTGGAGTGGGTGGCACTTATATCATATGATGAGAGACTAAATACATACGACACTCCGG 669
Db 167 LeuGIuIrPMeIeGIyTrPleIaSnIrHrIaStnGIyGIuProThrYrIaIaSpSerPhe 186
QY 670 AAGGGCGGATTCACATCTCCAGAGCACTTCCAGAGACGAGTGTATTAATAATGAAC 729
Db 187 IyGIyArGIaInPheThrPheSerIeIuAaSpSerIyAsnIthrAlaIyIreIuGIaInIleAa 206
QY 730 AGCTTGAAGACTGAGAGACAGCGCTGTCTATTACTGTGCAAGANTCAGACCTGTTGGGT 789
Db 207 SerIeIuArGIaInGIuAspThraIaValIyRpeCYaThArG-----Arg 221
QY 790 GACTATGACACACTACGAGTTTGAGCGTCTGGGGCAAGGAGACACCGGTACCGTCTCC 849
Db 222 GIyTrYrAspIrPTrYrPhe-----AspValIrPGIyGIaInGIyThrThrValIaIaSer 239
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QY 850 TCA 852
Db 240 Ser 240

RESULT 15
US-08-839-765-147
/ Sequence 147, Application US/08839765
/ Patent No. 614631
/ GENERAL INFORMATION:
/ APPLICANT: Better, Marc D.
/ APPLICANT: Carroll, Stephen F.
/ APPLICANT: Studika, Gary M.
/ TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
/ PROTEINS
/ NUMBER OF SEQUENCES: 169
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSER: McAndrews, Held & Malloy, Ltd.
/ STREET: 500 West Madison Street, 34th floor
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60661
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/839,765
/ FILING DATE: 15-APR-1997
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/425,336
/ FILING DATE: 18-APR-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/064,691
/ FILING DATE: 12-MAY-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/988,430
/ FILING DATE: 09-DEC-1992
/ APPLICATION DATA:
/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 19-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/707-9155
/ TELEFAX: 312/707-8889
/ INFORMATION FOR SEQ ID NO: 147:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 240 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-839-765-147

Alignment Scores:
Pred. No.: 1,46e-61 Length: 240
Score: 827.50 Matches: 161
Percent Similarity: 75.86% Conservative: 37
Best Local Similarity: 61.69% Mismatches: 42
Query Match: 48.31% Indels: 21
DB: 3 Gaps: 5

US-09-194-164-13 (1-918) x US-08-839-765-147 (1-240)
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OY 70 GATATTGTTGACGAGCTCCAGGACCCCTGTTTGTTCACAGGGAAGAAGCCACC 129
Db ||||| :||| ||||| ||||| :||| ||||| |||||
OY 130 CTCTCCGACGAGCCAGTCAGAGTATTAGACGACTTACCTGATCCAGACAGAAA 189
Db ||||| :||| ||||| ||||| :||| ||||| |||||
OY 21 IletHrCyArGAlaSerInAspIle---AsnSerTyrLeuSerTrpPheGlnGlnYs 39
Db ||||| :||| ||||| ||||| :||| ||||| |||||
OY 190 CCTGGCCAGGCTCCAGGCTCTCATCTATGTGTGATCCACAGGCGCATGGCATGCCA 249
Db ||||| :||| ||||| ||||| :||| ||||| |||||
OY 40 ProGlyLysAlaProLysThrLeuIleTyrArgAlaAsnArgLeuGlnSerGlyValPro 59
Db ||||| :||| ||||| ||||| :||| ||||| |||||
OY 250 GACAGGTTGAGTGGCGGTCCGGGAGAGACTTCACTCCACATCAGTACAGTAGAG 309
Db ||||| :||| ||||| ||||| :||| ||||| |||||
OY 60 SerArgPheSerGlySerGlyThrAspTyrThrLeuThrIleSerSerLeuGln 79
Db ||||| :||| ||||| ||||| :||| ||||| |||||
OY 310 CCTGAAGATTTTGCAGTATTACTGTACAGAGTATGATGCTCACCCTCAGACACTCAG 369
Db ||||| :||| ||||| ||||| :||| ||||| |||||
OY 80 TyrGluAspPheGlyIleTyrTyrCysGlnGlnTyrAspGluSerProIlePhe----- 96
Db ||||| :||| ||||| ||||| :||| ||||| |||||
OY 370 ATCACTTTGGCGGAGGAGCAAGAGTGAAGATCAACGAACGTGGCTGCACCATCTGTC 429
Db ||||| :||| ||||| ||||| :||| ||||| |||||
OY 97 ---ThrPheGlyGlyGlyThrLysLeuGluMetLys----- 107
Db ||||| :||| ||||| ||||| :||| ||||| |||||
OY 430 TCTGGCGGTGGGCTCCGAGGTGGTGTGATCAGGTGAGGTGGCTCCAGGTGACGCTG 489
Db ||||| :||| ||||| ||||| :||| ||||| |||||
OY 108 ---GlyGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlySerGlyGlyLeu 126
Db ||||| :||| ||||| ||||| :||| ||||| |||||
OY 490 GTGAGACTGCGGAGGAGCGGTGCTCCAGCTGGAGAGGTCCCTGAGACTCTCTGTGAGCC 549
Db ||||| :||| ||||| ||||| :||| ||||| |||||
OY 127 ValGlnSerGlyGlyGlyLeuValLysProGlyGlySerValArgIleSerCysAlaAla 146
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OY 147 SerGlyTyrThrPheThrAsnTyrGlyMetAsnTrpValArgGlnAlaProGlyLysGly 166
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OY 610 CTGGAGTGGGTGGCACTTATCATATGATGAGAGCACTAAATACTACCGACACTCCGTG 669
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OY 167 LeuGluTrpMetGlyTyrIleAsnThrIleThrGlyGluProThrTyrAlaAspSerPhe 186
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OY 670 AAGGCCGATTCACCATCTCCAGAGACACTTCCAGAGACAGCGGTATCTAAATAATGAAC 729
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OY 187 LysGlyArgPheThrPheSerLeuAspSerLysAsnThrAlaTyrLeuGlnIleAsn 206
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OY 207 SerLeuArgAlaGluAspThrAlaValTyrPheCysThrArg-----Arg 221
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OY 222 GlyTyrAspTrpIlePhe-----AspValTrpGlyGlnGlyThrThrValThrValSer 239
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Search completed: February 18, 2005, 08:47:44  
Job time : 28.5 secs

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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: February 18, 2005, 08:38:58 / Search time 203 Seconds  
(without alignments)  
2959.678 Million cell updates/sec

Title: US-09-194-164-13

Perfect score: 1713  
Sequence: 1 GAATTCATGAAAAAAGCGC.....ATCACCATTAGTGAAGCTT 918

Scoring table:  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1380268 seqs, 327241040 residues  
Total number of hits satisfying chosen parameters: 2760536

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Database : Published Applications AA:\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result Query

No.	Score	Match	Length	DB	ID	Description
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2	1573	91.8	304	15	US-10-651-453-14	Sequence 14, Appl
3	1451.5	84.7	287	10	US-09-782-397-17	Sequence 17, Appl
4	1451.5	84.7	287	15	US-10-651-453-17	Sequence 17, Appl
5	928	54.2	352	10	US-09-203-958A-2	Sequence 2, Appl
6	926.5	54.1	456	15	US-10-634-862-11	Sequence 11, Appl
7	892	52.1	283	9	US-09-983-580-6	Sequence 6, Appl
8	892	52.1	283	9	US-09-985-442-6	Sequence 6, Appl
9	887	51.8	263	9	US-09-956-086-3	Sequence 3, Appl
10	887	51.8	263	9	US-09-956-087-3	Sequence 3, Appl
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13	863.5	50.4	277	15	US-10-422-628-14	Sequence 43, Appl
14	857.5	50.1	279	15	US-10-409-938-21	Sequence 21, Appl
15	849.5	49.6	252	15	US-10-423-847-10	Sequence 10, Appl
16	849.5	49.6	252	15	US-10-423-847-14	Sequence 14, Appl
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18	849.5	49.6	254	15	US-10-423-847-17	Sequence 17, Appl
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20	827.5	48.3	240	14	US-10-127-890-147	Sequence 147, Appl
21	824.5	48.1	247	15	US-10-423-847-13	Sequence 13, Appl
22	824	48.1	443	13	US-10-006-773-2	Sequence 2, Appl
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24	810	47.3	4852	15	US-10-412-406-33	Sequence 14, Appl
25	808.5	47.2	409	15	US-10-353-121-14	Sequence 14, Appl
26	807.5	47.1	502	16	US-10-679-620-88	Sequence 88, Appl
27	806.5	47.1	663	15	US-10-412-406-32	Sequence 32, Appl
28	805	47.0	408	15	US-10-353-721-15	Sequence 15, Appl
29	803.5	46.9	252	9	US-09-971-543-1	Sequence 1, Appl
30	784.5	45.8	364	16	US-10-829-388-11	Sequence 11, Appl
31	784.5	45.8	370	16	US-10-829-388-1	Sequence 1, Appl
32	784	45.8	271	10	US-09-226-157-4	Sequence 4, Appl
33	784	45.8	374	14	US-10-335-394-15	Sequence 15, Appl
34	779.5	45.5	491	13	US-10-011-125-2	Sequence 2, Appl
35	777.5	45.4	543	14	US-10-207-655-146	Sequence 146, Appl
36	773	45.1	556	14	US-10-207-655-268	Sequence 268, Appl
37	770	45.0	296	15	US-10-418-182-2	Sequence 2, Appl
38	769.5	44.9	492	14	US-10-207-655-344	Sequence 344, Appl
39	767.5	44.8	543	14	US-10-207-655-345	Sequence 345, Appl
40	766	44.7	298	9	US-09-883-758-2	Sequence 2, Appl
41	762.5	44.5	431	14	US-10-013-173-4	Sequence 4, Appl
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44	761	44.4	258	14	US-10-207-655-343	Sequence 343, Appl
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## ALIGNMENTS

RESULT 1  
US-09-782-397-14  
; Sequence 14, Application US/09782397  
; Publication No. US20030021779A1  
; GENERAL INFORMATION:  
; APPLICANT: Dan, Michael D.  
; Kaplan, Pradipt K.  
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT  
SPECIFICALLY DIRECT CANCER CELLS, NUCLEOTIDES ENCODING THE  
FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND  
DETECTION OF CANCERS  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
ADDRESS: Morrison & Foerster LLP  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/782,397  
FILING DATE: 13-Feb-2001  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/862,124  
FILING DATE: 1997-05-22  
ATTORNEY/AGENT INFORMATION:  
NAME: Lehnhardt, Susan K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 31608-20001.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 304 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-09-782-397-14

Alignment Scores:  
Pred. No.: 1,93e-103 Length: 304  
Score: 1573.00 Matches: 302  
Percent Similarity: 100.00% Conservative: 0  
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Query Match: 91.83% Indels: 0  
DB: 10 Gaps: 0

US-09-194-164-13 (1-918) x US-09-782-397-14 (1-304)

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DB 1 GluPheMetIysThrAlaIleAlaValAlaLeuAlaGlyPheAlaThrVal 20  
QY 61 GCCGAGCCGATATGTGTGACGAGCTCCAGGACCCCTGTTCTCCAGGGGAA 120  
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QY 121 AGAGCCACCCCTCCCGGAGGGGCGAGTCAAGTTCAGACCCCTGTTCTCCAGGGGAA 180  
DB 41 ArgAlaThrLeuSerCysArgAlaSerGlnSerValSerSerSerThrLeuAlaTrpTyr 60  
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DB 61 GlnGlnIleProGlyGlnAlaProAlaGlnLeuIleTyrGlyAlaSerThrArgAlaThr 80  
QY 241 GCGATGCCAGACAGGTTCAAGTGGAGTGGCTCCGGGACAGACTTCACTCCACATCACT 300  
DB 81 GlyMetProAspArgPheSerGlySerGlyThrAspPheThrLeuThrIleSer 100  
QY 301 AGACTGAGCGCTGAATTTTGCAGGTATTACTGTCCACAGCTAAGTGCTGCTCACTCG 360  
DB 101 ArgLeuGlnIleProGlnAspPheAlaValTyrCysGlnGlnTyrGlySerSerProGln 120  
QY 361 ACACTCAGATCACTTTCGCGGAGGAGCAACAGTGGAGATCAACGAACTGGCTGCA 420  
DB 121 ThrProGlnIleThrPheGlyGlyGlyThrIleValGlnIleAspArgThrAlaAla 140  
QY 421 CCATCTGTCTTGGCGGTGGCGGTTCCGAGGTGGTGCATCAGTGGAGTGGCTCCAG 480  
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QY 481 GTGCACTGTGTGAGTCTGGGGAGGCGGTCCAGCCGCGGAGGCTCCGAGATCTCC 540  
DB 161 ValGlnIleValGlnIleSerGlyGlyGlyValValGlnIleProGlyArgSerLeuArgLeuSer 180

QY 541 TGTGACGCTTCGATTCCTCCCTTCAGAACCTTTGCTATGCACTGGGTCCGCCAGGCTCTA 600  
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QY 901 CACCAT 906  
DB 301 HisHis 302

RESULT 2  
US-10-651-453-14

Sequence 14, Application US/10651453  
Publication No. US20040091464A1  
GENERAL INFORMATION:  
APPLICANT: Dan, Michael D.  
APPLICANT: Malci, Pradipt K.  
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT SPECIFICALLY DETECT CANCER CELLS.  
TITLE OF INVENTION: NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHETIC  
FILE REFERENCE: 316082000103  
CURRENT APPLICATION NUMBER: US/10/651, 453  
CURRENT FILING DATE: 2003-08-29  
PRIOR APPLICATION NUMBER: US 09/782,397  
PRIOR FILING DATE: 2001-02-13  
PRIOR APPLICATION NUMBER: US 08/862,124  
PRIOR FILING DATE: 1997-05-22  
PRIOR APPLICATION NUMBER: US 08/657,449  
PRIOR FILING DATE: 1996-05-22  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 14  
LENGTH: 304  
TYPE: PRT  
ORGANISM: Homo Sapiens  
US-10-651-453-14

Alignment Scores:  
Pred. No.: 1,93e-103 Length: 304  
Score: 1573.00 Matches: 302  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 91.83% Indels: 0  
DB: 15 Gaps: 0

US-09-194-164-13 (1-918) x US-10-651-453-14 (1-304)

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DB 21 AlaGlnAlaAspIleValLeuThrGlnSerProGlyThrLeuSerLeuSerProGlyGln 40

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421 CCATCTGTCTCTGGCGGCTGGCGGCTTCGGAGGTGTGTGATCAGTGGAGTGGCTCCAG 480  
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481 GTGCGAGCTGTGAGTCTGGGGGAGCGCTGTCCAGCTCGGAGGTCCCTGAGACTTCC 540  
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541 TGTGAGACCTCTGATTCCTCCCTTCAAGAGCTTGTGATGACCTGGGTCGGCAGGCTCTA 600  
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781 CTGTGGGTGATATGACCACTACTACGCTTGTGACGCTCTGGGCAAGGAGCACAGCTC 840  
261 LeuLeuGlyAspTyrAspHisIleTyrGlyLeuAspValTrpGlyLysGlyThrThrVal 280  
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301 HisHis 302

RESULT 3  
US-09-782-397-17  
Sequence 17, Application US/09782397  
Publication No. US20030021779A1  
GENERAL INFORMATION:  
Applicant: Dan, Michael D.  
Maitl, Pradipt K.  
Kaplan, Howard A.  
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND DETECTION OF CANCERS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster LLP  
STREET: 755 Page Mill Road

CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/782,397  
FILING DATE: 13-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/862,124  
FILING DATE: 1997-05-22  
ATTORNEY/AGENT INFORMATION:  
NAME: Lehnhardt, Susan K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 287 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
US-09-782-397-17  
Alignment Scores:  
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Score: 1451.50 Matches: 283  
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Best Local Similarity: 93.71% Mismatches: 2  
Query Match: 84.73% Indels: 17  
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DB 41 ArgAlaThrLeuSerCysArgAlaSerGlnSerValSerSerSerThrLeuAlaTrpTyr 60  
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QY 241 GGCATGCCAGACAGGTTGAGTGGCAGTGGGTCGGAGACAGACTTCACTCCACCATCAGT 300  
DB 81 GlyMetProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSer 100  
QY 301 AGACTGAGACCTGGAAGATTTTGCAGTGTATTACTGTACAGCATATAGTATAGTACCTCG 360  
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DB 121 ThrProGlnIleThrPheGlyGlyTyrIleLysValGlnIleLysArgThrValAlaAla 140  
QY 421 CCATCTGTCTCTGGCGGCTGGCGGCTTCGGAGGTGTGTGATCAGTGGAGTGGCTCCAG 480

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Db 141 -----Serglysin 143
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QY 541 TGTGCAAGCGCTGAGATTCCTCCAGAACCTTGCTATGACACTGGGTCGGCAGGCTCA 600
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Db 184 GlyIysGlyLeuGlnTrpValAlaValIleSerTyrAspGlySerThrIysTyrAla 203
QY 661 GACTCGTGAAGGCGGATTCACCATCTCCAGAGACATTCAGAGAACCGGTATCTA 720
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Db 224 LysMetAsnSerLeuArgThrGluAspThrAlaValTyrTyrCysAlaArgAspGlnSer 243
QY 781 CTGTTGGGTGACTATGACCACTACTACGGTTTGAAGTGGGGCAAGGACCAAGCTC 840
Db 244 LeuLeuGlyAspTyrAspHisTyrTyrGlyLeuAspValTyrGlyIysGlyThrVal 263
QY 841 ACCGTCCTCTCAGATCCGAAACAAAACGTGATCAGCGAAGAGATCTGAACCATCACCAT 900
Db 264 ThrValSerSerGlySerGlnGlnIysLeuIleSerGlnGlyAspLeuAsnHisHis 283
QY 901 CACCAT 906
Db 284 HisHis 285

RESULT 4
US-10-651-453-17
; Sequence 17, Application US/10651453
; Publication No. US20040091484A1
; GENERAL INFORMATION:
; APPLICANT: Dan, Michael D.
; APPLICANT: Maiti, Pradip K.
; APPLICANT: Kaplan, Howard A.
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT SPECIFICALLY DETECT CANCER CELLS.
; TITLE OF INVENTION: DETECTION OF CANCERS
; FILE REFERENCE: 316082000103
; CURRENT APPLICATION NUMBER: US/10/651,453
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US 09/782,397
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: US 08/862,124
; PRIOR FILING DATE: 1997-05-22
; PRIOR APPLICATION NUMBER: US 08/657,449
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-651-453-17

Alignment Scores:
Pred. No.: 8,12e-95 Length: 287
Score: 1451.50 Matches: 283
Percent Similarity: 93.71% Conservative: 0
Best Local Similarity: 93.71% Mismatches: 17
Query Match: 84.73% Indels: 2
DB: 15 Gaps: 1

US-09-194-164-13 (1-918) x US-10-651-453-17 (1-287)
QY 1 GAATTCATGAAAAAACCCGCTATCGGATCGCAGTTGCACTGGCTTGCTACCGTT 60
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Db 1 GluPheMetCysIysThrAlaIleAlaIleAlaValAlaLeuAlaGlyPheAlaThrVal 20
QY 61 GCGCAGCGCATATTGTGTGACGCAAGTCTCCAGGACCCCTGTCTTGTCTCCAGGGAA 120
Db 21 AlaGlnAlaAspIleValLeuThrGlnSerProGlyThrLeuSerLeuSerProGlyGln 40
QY 121 AGAGCAGCCCTCTCCGAGGGCCAGTGCAGAGTGTATGATAGCTACTTACCGCTGATC 180
Db 41 ArgAlaThrLeuSerCysArgAlaSerGlnSerValSerSerTyrLeuAlaTrpTyr 60
QY 181 CAGCAAAACCTGGCCAGGCTCCAGGCTCTCATCTATAGTGCAATCCACAGGCGCACT 240
Db 61 GlnGlnIysProGlyGlnAlaProArgLeuLeuIleTyrGlyAlaSerThrArgAlaThr 80
QY 241 GGCATGCCAAGACAGTTCAAGTGCAGTGGGTCCGGAGACAGACTTCACTCAACCATCAGT 300
Db 81 GlyMetProAspArgPheSerSerGlySerGlyIysGlyThrAspPheThrLeuThrIleSer 100
QY 301 AGACTGAGCGCTGAAGATTTTGGCAGTGTATTACTGTACGAGTATGTAGGCTCACTCAG 360
Db 101 ArgLeuGlnProGluAspPheAlaValTyrTyrCysGlnGlnIlyTyrGlySerSerProGln 120
QY 361 ACACCTCAGATCACTTTCGGCGGAGGAGCAAGGTGAGATCAACAGAACTGTGGCTGCA 420
Db 121 ThrProGlnIleThrPheGlyGlyGlyThrIysValGlnIleIysArgThrValAlaAla 140
QY 421 CCATCTGTCTCTGGCGGTGGCGGTTCCGAGGTGTGATCAGGTGAGGTGGCTCCAG 480
Db 141 -----Serglysin 143
QY 481 GTGCAGCTGTGAGTCTGGGGGAGGCGTGTCCAGCCTTGAGAGTCCCTGAGACTGCC 540
Db 144 ValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeuSer 163
QY 541 TGTGCAAGCGCTGAGATTCCTCCAGAACCTTGCTATGACTGTGCGCAGGCTCTA 600
Db 164 CysAlaAlaSerGlyPheProPheArgSerPheAlaMetHisTrpValArgGlnAlaLeu 183
QY 601 GGCAAGAGGCGTGGAGTGGGCGACTTATATCATATGATGAGAGCACTAAATACTACGCA 660
Db 184 GlyIysGlyLeuGlnTrpValAlaValIleSerTyrAspGlySerThrIysTyrAla 203
QY 661 GACTCGTGAAGGCGGATTCACCATCTCCAGAGACATTCAGAGAACCGGTATCTA 720
Db 204 AspSerValIysGlyArgPheThrIleSerArgAspThrSerIysAsnThrValTyrLeu 223
QY 721 AAAATGAACAGCTGAGAACTGAGGACAGGCGTGTCTATTACTGTGCGAGAGATCAGAGC 780
Db 224 LysMetAsnSerLeuArgThrGluAspThrAlaValTyrTyrCysAlaArgAspGlnSer 243
QY 781 CTGTTGGGTGACTATGACCACTACTACGGTTTGAAGTGGGGCAAGGACCAAGCTC 840
Db 244 LeuLeuGlyAspTyrAspHisTyrTyrGlyLeuAspValTyrGlyIysGlyThrVal 263
QY 841 ACCGTCCTCTCAGATCCGAAACAAAACGTGATCAGCGAAGAGATCTGAACCATCACCAT 900
Db 264 ThrValSerSerGlySerGlnGlnIysLeuIleSerGlnGlyAspLeuAsnHisHis 283
QY 901 CACCAT 906
Db 284 HisHis 285

RESULT 5
US-09-203-958A-2
; Sequence 2, Application US/09203958A
; Publication No. US20030039641A1
; GENERAL INFORMATION:
; APPLICANT: KELLER, Tibor
; APPLICANT: GOLDSTEIN, Joel
; APPLICANT: GRAZIANO, Robert
; APPLICANT: DEO, Yashwant M.
; TITLE OF INVENTION: CELLS EXPRESSING ANTI-FC RECEPTOR
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QY 283 TTCACTCTCAACATCACTGAGACCTGGAAGATTTCGATGATTAATCTGACGAC 342
    |||||
    :
Db 101 PheThrLeuThrIleSerSerValGlnAlaAspLeuAlaValTyrCysGlnAsn 120
    |||||
    :
QY 343 TATGATGATCACTCACTGAGACCTGAGATCTTGGCGGAGGAGGACCAAGGTGGAGATC 402
    |||||
    :
Db 121 AspTyrSerAsnPro-----LeuThrPheGlyGlyThrTyrSleuGlnLeu 136
    |||||
    :
QY 403 AAACGAATGCTGGCTGACCATCT-----GTCTCTGGCGGT 438
    |||||
    :
Db 137 LysArgAlaGlyGlyGlySerGlyGlyGlyGlySerGlyGlyGlySerGlyGly 156
    |||||
    :
QY 439 GGGGGTTCGGAGGTGTGATCAAGTGGAGGCTCCAGGTGACGCTGTGGAGTCT 498
    |||||
    :
Db 157 GlyGlySerGlyGlyGlySerGlyGlyGlyGlySerGlyGlyGlyGlyGlnLeuValGlnSer 176
    |||||
    :
QY 499 GGGGAGGCGGTGGCTGACGCTGGGAGGTCCCTGAGACTCTCTGTGACGCTCTGAGATTC 558
    |||||
    :
Db 177 GlyGlyAspLeuValLysProGlyGlySerLeuLysLeuSerCysAlaAlaSerGlyPhe 196
    |||||
    :
QY 559 CCTTCGAAGCTTTGCTATGACCTGGGTCGCGCAGGCTCTAGGCAAGGGCTGAGATGG 618
    |||||
    :
Db 197 SerPheSerSerTyrGlyMetSerTyrValArgGlnThrProAspLysArgLeuGlnTyr 216
    |||||
    :
QY 619 GTGGCAGTTATATCATATGATGAGAGCACTAAATACAGACACTCCGTGAAGGGCCGA 678
    |||||
    :
Db 217 ValAlaThrIleSerAsnGlyGlyGlyTyrThrTyrTyrProAspSerValLysGlyArg 236
    |||||
    :
QY 679 TTCACATCTCCAGAGACACTTCCAGAGACAGCGGTGATCTAAATAATGAACAGCTGAG 738
    |||||
    :
Db 237 PheThrIleSerThrArgAspAsnAlaLysAsnThrLeuGlnMetSerSerLeuLys 256
    |||||
    :
QY 739 ACTGAGAGACGCGCTGTCTATTACTGTGCGAGAGATGAGAGCTGTGGGTGATATGAC 798
    |||||
    :
Db 257 SerGlnAspSerAlaMetTyrTyrCysAlaArgArgGlnArg-----TyrAsp 272
    |||||
    :
QY 799 CACTACGAGGTTTGACGCTGCTGGGGCAAGGAGACGCTCACCGTCTCTAGAGATCC 858
    |||||
    :
Db 273 Gln---AsnGlyPheAlaTyrTyrGlyGlnGlyThrLeuValThrValSerAlaSerGly 291
    |||||
    :
QY 859 GAA 861
    |||||
    :
Db 292 Gln 292

RESULT 7
US-09-983-580-6
; Sequence 6, Application US/09983580
; Patent No. US20020151061A1
; GENERAL INFORMATION:
; APPLICANT: Filipula, David R.
; APPLICANT: Meng, Maoliang
; TITLE OF INVENTION: NO. US20020151061A1 Method for Targeted Delivery of Nucleic Acids
; FILE REFERENCE: 0977.2300002
; CURRENT APPLICATION NUMBER: US/09/983,580
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 09/420,592
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/104,949
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Kabat
; NAME/KEY: UNSURE
; LOCATION: (232)
; OTHER INFORMATION: May be any amino acid.
```

```
; NAME/KEY: UNSURE
; LOCATION: (234)
; OTHER INFORMATION: May be any amino acid.
; NAME/KEY: UNSURE
; LOCATION: (239)
; OTHER INFORMATION: May be any amino acid.
US-09-983-580-6

Alignment Scores:
Pred. No.: 4.27e-55 Length: 283
Score: 892.00 Matches: 181
Percent Similarity: 76.92% Conservative: 29
Best Local Similarity: 66.30% Mismatches: 47
Query Match: 52.07% Indels: 16
DB: 9 Gaps: 5

US-09-194-164-13 (1-918) x US-09-983-580-6 (1-283)

QY 70 GATATTGTGTGACGACATCTCCAGACCCCTGTTGTCTCCAGGGGAAAGACCACC 129
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    :
Db 1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20
    |||||
    :
QY 130 CTCTCTCAGAGGCGCAGTCAGAGTGT-----AGTAGCAGCTACTTACCTGTATCCAG 183
    |||||
    :
Db 21 IleThrCysArgAlaSerGlnSerLeuValSerIleSerAsnTyrLeuAlaTyrPyrGln 40
    |||||
    :
QY 184 CAGAAACCTGGCAGGCTCCAGGCTCCTCATCTATGTGTGATCCACACAGGCGCACCTGGC 243
    |||||
    :
Db 41 GlnLysProGlyLysAlaProLysLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGly 60
    |||||
    :
QY 244 ATGCCAGACAGGTTGAGGAGGAGGTCGCGGAGACAGCTTCACTCAGATCAGTGA 303
    |||||
    :
Db 61 ValProSerArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSer 80
    |||||
    :
QY 304 CTGAGCCTGAAGATTGTGACGTGATTAATCTGACAGATGAGTGAAGTCACTCAGACA 363
    |||||
    :
Db 81 LeuGlnProGlnAspPheAlaThrTyrTyrCysGlnGlnTyrAsnSer-----Leu 97
    |||||
    :
QY 364 CCTCAGATCACTTTGGCGGAGGAGCAAGGTGAGATCAACGAACTGTGGCTGACCA 423
    |||||
    :
Db 98 ProGlnTyrThrPheGlyGlnGlyThrLysValGlnIleLysGlySer----- 113
    |||||
    :
QY 424 TCTGTCTGGCGGCGGTGCGAGGTGAGTGGATGAGGAGGTGCTCCAGGTG 483
    |||||
    :
Db 114 -----ThrSerGlySerGlyLysProGlySerGlyGlnGlySerThrLysGlyGlnVal 131
    |||||
    :
QY 484 CAGCTGTGAGATCTGCGGAGGAGCGTGTGTCAGGCTCGGAGATCCCTGAGACTCTCTGT 543
    |||||
    :
Db 132 GlnLeuValGlnSerGlyGlyGlyLeuValGlnProGlyGlySerLeuArgLeuSerCys 151
    |||||
    :
QY 544 GAGCCTCTGATTCCTTTCAGAAAGCTTGTCTATGACCTGGGTCCGACAGCTCTAGGC 603
    |||||
    :
Db 152 AlaAlaSerGlyPheThrPheSerSerTyrAlaMetSerTyrValArgGlnAlaProGly 171
    |||||
    :
QY 604 AAGGGCTGAGAGTGGGTGAGTTATATCA-----TATGATGGAAGACATAAATATCAC 657
    |||||
    :
Db 172 LysGlyLeuGlnTyrPheValSerValIleSerGlyLysThrAspGlyGlySerThrTyrTyr 191
    |||||
    :
QY 658 GCAGACTCGTGAAGAGGCGCATTCACATCTCCAGAGACACTTCCAGAGACAGGTGTAT 717
    |||||
    :
Db 192 AlaAspSerValLysGlyArgPheThrIleSerThrArgAspAsnSerLysAsnThrLeuTyr 211
    |||||
    :
QY 718 CTAATAATGAACAGCTGAGAACTGAGAGACAGGCTGTCTTATCTGTGCGAGATCAG 777
    |||||
    :
Db 212 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyrTyrCysAlaArgGlyArg 231
    |||||
    :
QY 778 -----AGCCTGTTGGTGAATGATCAACACTACTGAGTGTGGAGGCAAA 828
    |||||
    :
Db 232 ***Gly***SerLeuSerGly***TyrTyrTyrTyrHisTyrPheAspTyrTrpGlyGln 251
    |||||
    :
QY 829 GGGACACAGGTACCGTCTCTCAGAGATCCGAAACAAA 867
    |||||
    :
Db 252 GlyThrLeuValThrValSerSerLysLysLysLys 264
    |||||
    :
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## RESULT 8

US-09-985-442-6  
Sequence 6, Application US/09985442  
Patent No. US20020156248A1  
GENERAL INFORMATION:  
APPLICANT: Filipula, David R.  
APPLICANT: Wang, Maoliang  
APPLICANT: Whitlow, Marc D.  
TITLE OF INVENTION: NO. US20020156248A1 Method for Targeted Delivery of Nucleic Acid  
FILE REFERENCE: 0977.2300003  
CURRENT FILING DATE: 2001-11-02  
PRIOR APPLICATION NUMBER: 09/420,592  
PRIOR FILING DATE: 1999-10-19  
PRIOR APPLICATION NUMBER: 60/104,949  
PRIOR FILING DATE: 1998-10-20  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 283  
TYPE: PRF  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Kabat  
NAME/KEY: UNSURE  
LOCATION: (232)  
OTHER INFORMATION: May be any amino acid.  
NAME/KEY: UNSURE  
LOCATION: (234)  
OTHER INFORMATION: May be any amino acid.  
NAME/KEY: UNSURE  
LOCATION: (239)  
OTHER INFORMATION: May be any amino acid.  
US-09-985-442-6

## Alignment Scores:

Pred. No.:	4,27e-55	Length:	283
Score:	892.00	Matches:	181
Percent Similarity:	76.92%	Conservative:	29
Best Local Similarity:	66.30%	Mismatches:	47
Query Match:	52.07%	Indels:	16
DB:	9	Gaps:	5

US-09-194-164-13 (1-918) x US-09-985-442-6 (1-283)

QY 70 GATATTGTGTGACGAGCTCCAGGCAACCTGCTTTGTCTCCAGGGGAAGAGCCACC 129  
DB 1 AaplleGlmMetThglNserProSerSerLeuSerAlaSerValGlyAapArgValThr 20  
QY 130 CTCTCTGAGGCGGAGCTCAGAGTGT-----AGTACAGCTACTTACCTGGTACAG 183  
DB 21 IletHrCyArgAlaSerSerLeuValSerIleSerAanTyIleuAlaTrpTyArgin 40  
QY 184 CAGAAACTGGCGAGGCTCCAGGCTCTCATCTATGTGTCATCCACGAGGCCACTGAC 243  
DB 41 GlnlySProGlyLylAlaProlySerLeuLeuIleTyAlaAlaSerSerLeuGlnSerGly 60  
QY 244 ATGCAGACAGGTTGAGTGGGAGTGGGTCGCGGACAGACAGACTCCTACCTCAGTACA 303  
DB 61 ValProSerArgPheSerSerIleSerGlySerGlyThrAapPheThrLeuThrIleSerSer 80  
QY 304 CTGAGAGCTGAGATTTTGTGACGTATTAATCTGTCAGACAGTATGATGCTCACCTGACA 363  
DB 81 LeuGlnProGlyAapPheAlaThrIleTyArgyGlnGlnIntlyAanSer-----Leu 97  
QY 364 CCTGAGATCACTTTGGCGGAGGAGCAAGGTGAGATTAACCAAGTCTGGCTGACACA 423  
DB 98 ProGluTrpThrPheGlyGlnGlyThrIleValGlnIleTyGlySer----- 113  
QY 424 TCTGTCTGGCGGTCGCGGCTCCGAGAGGTGATGATGAGTGGAGGTGCTCCAGAGTG 483

DB 114 -----ThSerGlySerGlyLysProGlySerGlyGlnGlySerThrIleGlyVal 131  
QY 484 CAGCTGTGAGACTTGGGGGAGGCGGTGTCCAGGCTGGAGAGTCCCTGAGACTCTCTGT 543  
DB 132 GlnLeuValGlnSerGlyGlyGlyLeuValGlnProGlyGlySerLeuArgLeuSerCy 151  
QY 544 GAGAGCTGTGAGTCCCTCCAGAACTTGTCTATGACACTGGGTCCGAGGCTCAGGC 603  
DB 152 AlaAlaSerGlyPheThrPheSerSerTyAlaMetSerTrpValArgGlnAlaProGly 171  
QY 604 AAGGCGCTGAGTGGGTGGGCTGATTAATCA-----TATGATGAGACACTAAATCA 657  
DB 172 LysGlyLeuGlnTrpValSerValIleSerGlyLysThrAapGlySerThrIleTy 191  
QY 658 GCAGACTCCGTGAAAGGCGGATTCACCATCTCCAGAGACACTTCCAAAGACAGGTGAT 717  
DB 192 AlaAapSerValIleGlyArgPheThrIleSerArgAapAanSerLysAanThrLeuTy 211  
QY 718 CTMAAAATGACAGCTGAGAACTGAGACAGGCTGTCTATTAATCTGTGCGAGATCAG 777  
DB 212 LeuGlnMetAanSerLeuArgAlaGlnAapThrAlaValIleTyIleCyAlaArgGlyArg 231  
QY 778 -----AGCTGTGGGTGACTATGACACTACTACAGTTTGACGTCGGGAGCA 828  
DB 232 \*\*\*Gly\*\*\*SerLeuSerGly\*\*\*TyTrpTyTrpIleTyIlePheAapTyTrpGlyGln 251  
QY 828 GGGACACGCTCAGCGTCTCTCAGAGATCCGACAAAA 867  
DB 252 GlyThrLeuValThrValSerSerIleLysLysLysLys 264

## RESULT 9

US-09-956-086-3  
Sequence 3, Application US/09956086  
Patent No. US2002015498A1  
GENERAL INFORMATION:  
APPLICANT: FILIPULA, DAVID  
APPLICANT: WANG, MAOLIANG  
APPLICANT: SHORR, ROBERT  
APPLICANT: WHITLOW, MARC  
LEE, LIHSYNG S.  
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS  
CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVE., NW, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/956,086  
FILING DATE: 20-Sep-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/069,821  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 60/063,074  
FILING DATE: 27-OCT-1997  
APPLICATION NUMBER: US 60/050,472  
FILING DATE: 23-JUN-1997  
APPLICATION NUMBER: US 60/044,449  
FILING DATE: 30-APR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: KIM, JUDITH U.  
REGISTRATION NUMBER: 40,679  
REFERENCE/DOCKET NUMBER: 0977.2280003  
TELECOMMUNICATION INFORMATION:



US-09-194-164-13	(1-918)	x	US-09-956-086-3	(1-263)
<p>TELEPHONE: (202) 371-2600  TELEFAX: (202) 371-2540  INFORMATION FOR SEQ ID NO: 3:  SEQUENCE CHARACTERISTICS:  LENGTH: 263 amino acids  TYPE: amino acid  STRANDEDNESS: single  TOPOLOGY: No. US20020155498A1 Relevant  MOLECULE TYPE: peptide  SEQUENCE DESCRIPTION: SEQ ID NO: 3:</p>				
<p>US-09-956-086-3</p>				
<p>Alignment Scores:</p>				
Pred. No.:	9,63e-55	Length:	263	
Score:	887.00	Matches:	180	
Percent Similarity:	77.24%	Conservative:	27	
Best local Similarity:	67.16%	Mismatches:	45	
Query Match:	51.78%	Indels:	16	
DB:	9	Gaps:	5	
<p>US-09-194-164-13 (1-918) x US-09-956-086-3 (1-263)</p>				
QY	70	GATATTGTGTAAAGAGTCTCCAGGCAACCCGTCTTGTCTCCAGGGGAAAGGCCACC	129	
DB	1	ASPIIIeGImeThrInserProSerSerLeuSerAlaSerValGlyAPaGValThr	20	
QY	130	CTCTCTGCAGGGCCAGTCAGAGTGT-----AGTACAGCTACTTACCTGGTACAG	183	
DB	21	ILeThrCyAArgAlaSerGlnSerLeuValSerIleSerAanTyrlaAlaIrrpGln	40	
QY	184	CAGAAACCTGGCCAGGCTCCAGGCTCCATCTATGTGCAATCCAGGAGCCACTGGC	243	
DB	41	GlnIlySerProGlyAlaProIlySerLeuLeuIleTyrlaAlaIleSerLeuGlnSerGly	60	
QY	244	ATGCCAGACAGTTCAGTGGCAGTGGGATCCGGAGACAGCTTCACTTCAACATCAGTGA	303	
DB	61	ValProSerArhpheserGlySerGlySerGlyThrAphethrIleuThrIleSerSer	80	
QY	304	CTGAGCCTGAAGATTTCAGAGTGTATTACTGTCAAGCATGTGGTAGCTCACTCAGACA	363	
DB	81	LeuGlnProGlnAphApehAlaThrTyrlTyrcysGlnGlnTyrlAanSer-----Leu	97	
QY	364	CCCTCAGATCACTTCCGCGGAGGAGGACCAAGGAGGAGATCAAAACGATCGGCGTCAACA	423	
DB	98	ProGlnIrrThrPheIlyGlnIlyThrIlyValGlnIleIlyGlySer-----Ily	113	
QY	424	TCTGTCTTGGCGGTGCGGTTCCGAGGTGGTGAATCAGGTGAGGTGGCTCCAGGTG	483	
DB	114	-----ThSerGlySerGlySerProGlySerGlyGlnIlySerThrIlyGlyIleVal	131	
QY	484	CAGCTGTGTGAAGTCGGGGGAGCGGTGTCCAGCTGGAGAGTCCCTGAACATCTCTGT	543	
DB	132	GlnIleValGlnSerIlyGlyIleValGlnProGlyIlySerLeuAlyLeuSerCys	151	
QY	544	GCAGCCTGTGAATCCCTTCAAGAGCTTGTGTATGCACTGGGTCGCCAGGCTTAGGC	603	
DB	152	AlaAlaSerGlyPheThrPheSerSerIlyrAlaMetSerIrrValaGlnAlaIrrGly	171	
QY	604	AAGGGCTTGAAGTGGGTGCGAGTTATATCA-----TATGATGGAAGCACTAATATCTAC	657	
DB	172	IlyGlyIleuGlnIrrPylValSerValIleSerGlyIlyStrApeGlyIlyGlnThrIlyTyrl	191	
QY	658	GCAGATCTCGTAAAGGCGGATTCACCAATTCGAGAGCACTTCCAGAAACAGGGTAT	717	
DB	192	AlaApeSerValIlyGlyIlyrPheThrIleSerIlyrApanSerIlyrAanThrIleTyrl	211	
QY	718	CTAAATTAACAACGCTTAGAACTGAGGACACGCGTGTCTATTACTGTGCAAGATACG	777	
DB	212	LeuGlnIleAanSerIleuAlyrAlaGlnApeThrAlaValTyrlTyrcysAlaIrrGlyIly	231	
QY	778	-----AGCTGTGGGTGAATATACCACTATACGTTTGGACGTCGGGGCAAA	828	
DB	232	***Gly***SerIleSerGly***TyrlTyrlTyrlIlyrIlyrPheApeTyrlTrrpGlyGln	251	

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Oy      829  GGAGCCAGCTCAGCTCTCTCA 852
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DB      252  GlythrlLeuValThrValSer 259

RESULT 10
US-09-956-087-3
; Sequence 3, Application US/09956087
; Patent No. US20020161201A1
; GENERAL INFORMATION:
APPLICANT: PILEPIA, DAVID
           WANG, MAOLIAN
           SHORR, ROBERT
           WHITLOW, MARC
           LEE, LISHYNG S.
TITLE OF INVENTION: CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/956,087
FILING DATE: 20-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/069,821
FILING DATE: 1998-04-30
APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997
APPLICATION NUMBER: US 60/044,449
FILING DATE: 30-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0977.2280003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-956-087-3

Alignment Scores:
Pred. No.:          9.63e-55          Length:          263
Score:              887.00             Matches:          180
Percent Similarity: 77.24%             Conservative:     27
Best Local Similarity: 67.16%           Mismatches:       45
Query Match:        51.78%             Indels:           16
DB:                 9                  Gaps:             5

US-09-194-164-13 (1-918) x US-09-956-087-3 (1-263)

Oy      70  GAAATGTGTTCAGCGAGTCTCCAGGACCCCTTCTTTGTCTCCAGGGGAAAGACACC 129
        .....:.....:.....:.....:.....:.....:.....:.....:.....
DB      1  AspllelInethrTgInserProSerSerLeuSerAlaSerValGlyAspArgValThr 20

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QY 130 CTCTCTGAGGGCCAGTCAAGTGT-----AGTACAGCTACTTACCTGTACCG 183
DB 21 ILEMTCYARXALASERISERLEUVALSERILLESERATRYLEUVALTRYRGIN 40
QY 184 CAGAAACCTGGCCAGGCTCCAGGCTCCATCTATAGTGATCCACAGGCGCACTGGC 243
DB 41 GINLYSPROGILYLYALALPROLYLEULEUILLERYALALASERISERLEUVALTRY 60
QY 244 ATCCAGACAGGTTCACTGGCAGTGGTCCGGACAGACTTCACTTCCATCCATCAGTACA 303
DB 61 VALPROSERARGPHEISERGLYSERGLYSERGLYTHNAPHEITHREUVALTRYR 80
QY 304 CTGGAGCCCTGAGATTTTTCAGTATTTCTGTCCAGCACTATGATAGCTACCTCAGACA 363
DB 81 LEUGINPPOGILUAPPHALATHRYTRYCYSGINGINTRYANSE-----LEU 97
QY 364 CCTCATCATCTTTCGGCCGAGGAGCAAGGTGAGATCAAGAACTGTGGCTGACCA 423
DB 98 PROGILUTPRTHRPHEGLYGINLYTHRYVALGILILEYGLYSER----- 113
QY 424 TCTGTCTGCGCGGTGGCGGTTCGGAGGTGGTGAAGTGAAGTGGCTCCAGGTG 483
DB 114 -----THSERGLYSERGLYSPROGLYSERGLYGLUGLYSERTHRYGLYVAL 131
QY 484 CAGCTGTGGAGTCTGGGGGAGCGGTGTCAGCTGGGAGGTCCCTGAGACTTCTCTGT 543
DB 132 GINLEUVALGINSERGLYGLYGLYLEUVALGINPROGLYGLYSERLEUARGLEUSERCYS 151
QY 544 GCAGCCTCTGATTCCTCCCTTCAGAGCTTGTATGACTGGGTCCGCGAGCTCAGGC 603
DB 152 ALAALASERGLYPHETHPHEISERERTYRALAMESETTRIPVALARGINLALPROGLY 171
QY 604 AAGGGCTGAGTGGGTGGGCACTTATATCA-----TATGATGAAGCACTAATAATAC 657
DB 172 LYEGILYGLUINUTRPVALSERVALILLESERGLYLYSTHAPGLYGLYSERTHRYTRYR 191
QY 658 GCAGCTCCCTGTAAGGGCCGATTCACCATCTCCAGAGACATTCAGAAACCGGTAT 717
DB 192 ALAASERVALYLYGLYARGPHEITHRILLESERARGAPASERISYASNTHRILEUVAL 211
QY 718 CTAAATAATGAACAGCTGGAACCTGAGACAGCGCTGTATTACTGTCGAGATGAG 777
DB 212 LEUGINMEASERLEUVALAGLUNAPHTHVALVALTRYTRYCYALALARGGLYARG 231
QY 778 -----AGCCTGTGGGTGATGATGACCACTACTACGAGTTTGAGAGTCTGGGCAAA 828
DB 232 ***GLY***SERLEUSERGLY***TYRTRYTRYTRYRHSYRPHASAPTRYTRPGLYGIN 251
QY 829 GGGACCAAGGTCAACCGTCTCCCTCA 852
DB 252 GLYTHREUVALTRYVALSERISER 259

RESULT 11
US-10-422-628-48
; Sequence 48, Application US/10422628
; Publication No. US20040014174A1
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; APPLICANT: MAYFIELD, Stephen P.
; APPLICANT: FRANKLIN, Scott E.
; TITLE OF INVENTION: EXPRESSION OF POLYPEPTIDES IN CHLOROPLASTS, AND COMPOSITIONS AND
; FILE REFERENCE: FOR EXPRESSING SAME
; CURRENT FILING DATE: 2003-04-23
; PRIOR FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/375,129
; PRIOR FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/434,957
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48

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; LENGTH: 630
; TYPE: PR
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Single-chain antibody
US-10-422-628-48

Alignment Scores:
Pred. No.: 2,856-53 Length: 630
Score: 866.50 Matches: 180
Percent Similarity: 76.12% Conservative: 24
Best Local Similarity: 67.16% Mismatches: 51
Query Match: 50.58% Indels: 13
DB: 15 Gaps: 4

US-09-194-164-13 (1-918) x US-10-422-628-48 (1-630)
QY 58 GTTGGCAG-----GCCGATATTGTGTGACGAGTCTCCAGGACCGCTGTCTGTCCA 114
DB 2 VALALAGINALALASERISERGLYUENHTRGINSERPROGLYTHREUSERLEUVALTRY 21
QY 115 GGGGAAGAGCCACCTCTCTGACAGGCGCAAGTCAAGTGTATGATGACACTTACGCC 174
DB 22 GLYUVALGALATHRLEUSERCYARGLALASERINSERVALSERISERLALTRYLEUALA 41
QY 175 TGTACCCAGCAGAAACCTGGCCAGGCTCCAGGCTCTCATATTATGATGATCCACAGG 234
DB 42 TRYTRYGINLILYSPROGLYGLINLALPROVGLLEUILLERYGLYALASERISERARG 61
QY 235 GCCACTGGCAGCCAGCAGGATTCAGTGGAGTGGGTCCGGGACAGACTTCACTCTCACCC 294
DB 62 ALATHRGILYILEPROASPARPHEISERGLYSERGLYSERGLYTHNAPPHETHRLEUVAL 81
QY 295 ATCACTAGACTGAGACCTGGAAGATTTTTCAGTGTATTACTGTCAAGATGATGATGATCA 354
DB 82 ILESERARGLEUGINUTRPGLUAPPHALATHRYTRYCYSGINGINTRYGLYARGSER 101
QY 335 CCTCAGACACTCAGATCACTTTCGGCGGAGGAGCAAGGTGAGATCAAGAACTGTG 414
DB 102 PRO-----THRPHGLYGLYGLYTHRYVALGILILEYVALRGTHTHR--- 115
QY 415 GCTGACCATCTGTCTGTGGCGGTGGCGGTTCGGAGGTGGTGAAGTGGAGTGGC 474
DB 116 -----SERISERGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLY 129
QY 475 TCCAGTGCAGCTGTGTGAGTCTGGGAGGCGGTGTCACAGCTGGGAGGTCCCTGAGA 534
DB 130 SERARGSERISERLEUGINLSERGLYALAGUVALYLYSPROGLYSERISERVALYLS 149
QY 535 CTCTCTGTGACGCTCTGGAATTCCTCTCAGAGCTTGTCTATGACACTGGTCCGCCAG 594
DB 150 VALSERCYLYSVALASERGLYGLYSERPHESERERTYRALALIASNTTRIPVALARGIN 169
QY 595 GCTTGAAGCAGGGGCTGAGTGGGTGAGTGGTCACTTATATGATGAGAAAGCACTAATAC 654
DB 170 ALAAGINGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLY 189
QY 655 TACGAGACTCCGTAAGAGGCGGATTCACCATCTCCAGACACTTCCAGAAACCGGTG 714
DB 190 TYRILAGINLYSPHEGLUAPPHARGLEUHTHRLALASERISERISERISERISERISER 209
QY 715 TATCTAAATAATGAACAGCTGGAACCTGAGACAGCGCTGTCTATTAATGTCGAGAGAT 774
DB 210 TYRMECTGINSERISERGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLY 229
QY 775 CAGAGCCGTGGTGGGATGATGACCACTACAGTGTGGAGTGGGCGGAGGAGGAGGAGG 834
DB 230 ALATYRMECTLEUGINUTRPOTHVALTHRALAGLYLEUAPVALTRPGLYLYGLYTHR 249
QY 835 ACGGTACCGTCTCTCAGATCC 858
DB 250 THRVALTHRVALSERPROALASER 257

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Db      83 1158rghleuGluproGluaphealAvalrTyrcyselmlnryglYargser 102
Qy      355 CCTCAGACACCTCAGATCACTTCGGCGAGGAGCCAGGTGAGATCAACGCACTGTG 414
Db      103 Pro-----ThrPheglYglYThrYValglulleyaargthr----- 116
Qy      415 GCTGACCACTGTGTCTCTGCGCGGTGCGGTTCCGAGGTGTGTGATCAGGTGAGGTGCG 474
Db      117 -----SerSerlYglYglYglYSerGlYglY-----GlyglYglYser 130
Qy      475 TCCAGAGTCAGGTGAGTGTGAGTGTGAGGAGGCGGTGCGAGTGTGAGGTCCTGAGAG 534
Db      131 SerArgSerleuGlunleuGlunleuGlYalagluValYelYelProGlySerSerValYs 150
Qy      535 CTCTCTGTGACAGCCTTGAGATTCCTCTCAGAGCTTGTCTAGATGCACTGGTCCGCGAG 594
Db      151 ValSerCyelYelAlaSerGlYglYSerPheSerSerTyAlaIlelethrYValargln 170
Qy      595 GCTTAGGCAAGGGGCTGAGAGTGGTGGGCACTTATTCATATGATGGAAGCACTAAATAC 654
Db      171 AlaGlnGlYglYglYleuGlunlurPmetGlYglYleuMeCProIlePheglYThrThrAen 190
Qy      655 TAGGAGACTCCGTGAAGGCGGATTCACATCTCCAGAGACACTTCCAAAGAACAGCGTG 714
Db      191 TyrAlaGlnLYpheGlunapArgleuThrIleThrAlaSpValSerThrSerThrAla 210
Qy      715 TATCTAAATGAAACAGCCTGAGAACTGAGACACGCGTGTCTATTACTGTGCGAGAGAT 774
Db      211 TyrMetGlnLeuSerGlYleuThrYrgluAepThrAlaMetYrTyrcyAlaIaargVal 230
Qy      775 CAGACCGCTTGGGTGATGATGACCACTACTACGTTTGACGCTGGGGCAAGGAGAC 834
Db      231 AlaTyrMetLeuGlunProThrValThrAlaGlYglYleuAaspValTrpGlYysglYthr 250
Qy      835 ACGGTACCGCTGCC 849
Db      251 ThrValThrValSer 255

RESULT 14
US-10-409-938-21
/ Sequence 21, Application US/10409938
/ Publication No. US20030219733A1
/ GENERAL INFORMATION:
/ APPLICANT: Clark et al.
/ TITLE OF INVENTION: ANTIBODY GENE TRANSFER AND RECOMBINANT AAV THEREFOR
/ FILE REFERENCE: 28335/39282
/ CURRENT APPLICATION NUMBER: US/10/409,938
/ CURRENT FILING DATE: 2003-04-09
/ PRIOR APPLICATION NUMBER: US 60/371,501
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 21
/ LENGTH: 279
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-409-938-21

Alignment Scores:
Pred. No.: 1,2e-52 Length: 279
Score: 857.50 Matches: 179
Percent Similarity: 73.36% Conservative: 22
Best Local Similarity: 65.33% Mismatches: 46
Query Match: 50.06% Indels: 27
DB: 15 Gaps: 6

US-09-194-164-13 (1-918) x US-10-409-938-21 (1-279)
Qy      67 GCCGATATGTGTGACGAGCTCCAGGACACCTGTCTTGTCTCCAGGAGGAAGAGCC 126
Db      21 AlaAapIleValleuThrInserProGlyThrLeuSerleuSerAlaGlYglunrGala 40

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Qy      127 ACCCTCTCTGAGAGGCCAGTCAAGTGTATTAGCACTACTTACCTGTGACGACAG 186
Db      41 ThrLeuSerCyAlaArgAlaSerGlnSerValSerSerGlySerleuAlaTrpYrglnGln 60
Qy      187 AAACGTGGCGAGAGCTCCCGAGGCTCTCATCTATGAGGATCCACAGGAGCCACTGAGCAT 246
Db      61 LysProGlnYglInAlaProArgleuLeuIleTyrglyAlaSerThrArgAlaThrYglIle 80
Qy      247 CCAAGACAGTTGATGAGCGATGAGGTTCGGAGACAGACTTCACTTCCATCACTAGTAGACTG 306
Db      81 ProAapArgPheSerGlYserGlYserGlYThrAapPheThrleuThrIleGlyArgleu 100
Qy      307 GAGCTTGAAGATTTTGCAGTGTATTACTGTTCAGCACTAGTAGTCACTCACTCAGACACT 366
Db      101 GlunProGluAapleuAlaValTyrcysGlnGlnTyrglyThrSerPro----- 117
Qy      367 CAGATCACTTTGCGGCGAGGAGCAAGGTGAGATCAACGAACTGTGCTGACCATCAT 426
Db      118 ---TyrThrPheGlYglYglYThrlySValAapIleYarg----- 130
Qy      427 GTCTGTGGCGGTGCGGTTCCGAGGTGTGATCAGGTGAGGTGC-----TCC 477
Db      131 -----GlyglYglYglYserGlYglYglYglYglYglYglYglYglYglYglYglYglY 148
Qy      478 CAGGTGACAGTGTGAGAGTCTGGGAGGCGGTGTCACCTGGGAGGTCCCTGAGACTC 537
Db      149 GlnValGlnLeuValGlnSerGlYalagluValYelYsProGlySerSerValGlnVal 168
Qy      538 TCCTGTGAGCCTGTGAGATTCCTCAGAACTTGTATGACACTGGGTCCGCGCAGGCT 597
Db      169 SerCylyAlaSerGlYglYThrPheSerMetYrglyPheAenThrPalArglnAla 188
Qy      598 CTAGGCAAGGCGCTGAGTGGTGGCAGTTATATCATATGATGAAAGCACTAAATATAC 657
Db      189 ProGlnHleGlYleuGlunlurPmetGlYglYleIleProIlePheGlYThrSerAenTy 208
Qy      658 GCGAGACTCCGTAAAGGCGGATTCACATCTCCAGAGACACTTCCAAAGAACGCGTGTAT 717
Db      209 AlaGlnLYpheArgglYArgValThrPheThrAlaAepGlnAlaThrSerThrAlaTy 228
Qy      718 TATTAATGAAACAGCCTGAGAACTGAGACACGCGTGTATTACTGTGCGAGAGATCAG 777
Db      229 MetGluLeuThrAaMetleuArgSerleuPheThrAlaValTyrcyAlaIaargAap--- 247
Qy      778 AGCCTGTGGGT-----GACTATGACCACTACTACGCT----- 810
Db      248 -----PheglYProAapTrpGlunAepGlYAspSerTyAspGlYserGlYarglYpHe 265
Qy      811 TTGACAGTCTGGGCGAAAGGACCAAGCTCACCGTCTCTCTCA 852
Db      266 PheAapPheTrpGlYglYglYThrleuValThrValSerSer 279

RESULT 15
US-10-423-847-10
/ Sequence 10, Application US/10423847
/ Publication No. US20040009166A1
/ GENERAL INFORMATION:
/ APPLICANT: FILIPULA, DAVID RAY
/ APPLICANT: YANG, KAREN
/ APPLICANT: BASU, AMARTYA
/ APPLICANT: WANG, MAOLIAN
/ TITLE OF INVENTION: SINGLE CHAIN ANTIGEN-BINDING POLYPEPTIDES FOR POLYMER
/ FILE REFERENCE: 213,1180
/ CURRENT APPLICATION NUMBER: US/10/423,847
/ CURRENT FILING DATE: 2003-04-25
/ PRIOR APPLICATION NUMBER: 09/791,578
/ PRIOR FILING DATE: 2001-02-26
/ PRIOR APPLICATION NUMBER: 09/791,540
/ PRIOR FILING DATE: 2001-02-26
/ PRIOR APPLICATION NUMBER: 09/069,842
/ PRIOR FILING DATE: 1998-04-30
/ PRIOR APPLICATION NUMBER: 60/044,449

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; PRIOR FILING DATE: 1997-04-30
; PRIOR APPLICATION NUMBER: 60/050,472
; PRIOR FILING DATE: 1997-06-23
; PRIOR APPLICATION NUMBER: 60/063,074
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: 60/067,341
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic 2-7-SC-1
; US-10-423-847-10
```

## Alignment Scores:

Pred. No.:	4,42e-52	Length:	252
Score:	849.50	Matches:	170
Percent Similarity:	72.04%	Conservative:	31
Best Local Similarity:	60.93%	Mismatches:	51
Query Match:	49.59%	Indels:	27
DB:	15	Gaps:	5

US-09-194-164-13 (1-918) x US-10-423-847-10 (1-252)

```

QY 70 GATATTGTGTGACGAGCTCTCCAGGACCCCTGTTGTTCTCCAGGGAGAAAGCCACC 129
    |||||  ::::|  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1 AepIIeGImerThrInSerProSerSerLeuSerAlaSerValGIyAspArgValThr 20
QY 130 CTCTCCTCGAGGCGCCAGTGAAGTGTAGAGCACTACTTACCTGGTACCGAGAGAA 189
    ::::|  ::::|  ::::|  ::::|  ::::|  ::::|  ::::|  ::::|  ::::|  ::::|
    21 IeThrCyArGAlaSerGlnGlyLe---ArgAsnTyrlneuLaTrpTyrgInGlnLys 39
QY 190 CCTGGCCAGGCTCCAGGCTCTCATCTATGTGATCCAGGCGCACTGGCATGCCA 249
    |||||  ::::|  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 40 ProGIyAlaProIySleuLeuIeTyrlAlaIaSerThrIeuGInSerGIyAlPro 59
QY 250 GACAGGTTCACTGGAGTGGGTCGGGAGACAACTTCACCTCCATCAGTAGACTGAG 309
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 60 SerArgPheSerGIySerGIySerGIyThrAspPheThrIeuThrIleSerSerIeuGIn 79
QY 310 CCTGAAGATTTCAGTGTATTACTGTCCAGCAGTATGTAAGTCACTCAGACCTCAG 369
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
    80 ProGIuAspValAlaThrTyrlCySgInArgIyTrAsnArgAlaPro----- 95
QY 370 ATCACTTTCGGCGGAGGAGCAAGGTGAGATCAAAAGCACTGGGCTGCACCATCTGTC 429
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 96 TyrThrPheGIyGlnGIyThrIyValGIuIleIySgIySer----- 109
QY 430 TCTGGCGGTGGCGGTTCCGAGGTTGGATCAAGTGAAGTGGCTCCAGGTGCAGCTG 489
    ::::|  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 110 ThrSerGIySerGIySproGIySerGIyGlnGIySerThrIySgIyGIuValGIuLeu 129
QY 490 GTGGAGTCTGGGGAGGCGGTGTCAGCTGGAGGTCCTTGAGATCTCTCTGTGCAGCC 549
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 130 ValGIuSerGIyGIyGIyIleuValGIuProGIyArgSerIeuArgIeuSerCySAlaIa 149
QY 550 TCTGATTCCTCCCTTCAGAGCTTTCATATGATGAGAGCACTAAATCTACGACAGCTCCG 609
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 150 SerGIyPheThrPheAspArgTyrlAlaMetHleTrpValArgGIuAlaProGIyIySgIy 169
QY 610 CTGAGAGTGGGTGAGCTTATATCATATGATGAGAGCACTAAATCTACGACAGCTCCG 669
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 170 LeuGIuTrpValSerAlaIleThrTrpAsnSerGIyHIsIleAspTyrlAlaPheSerVal 189
QY 670 AAGGGCCGATTCACCATCTCCAGAGACATTCGAGAGACAGGTGTATCTAAATATGAA 729
    ::::|  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 190 GIuGIyArgPheThrIleSerArgAspAsnAlaIyAsnSerIeuTyrlIeuGInMetAsn 209
QY 730 AGCTGAGAACTGAGAGCAAGGCTGTCTATTACTGTGCGAGAGATCAGAGCCCTGTGGGT 789
```

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Db 210 SerIeuAlaGAlaGIuAspThrAlaValTyrlTyrlCySAlaIySValSerTyrlIeu----- 227
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 790 GACTATGACCACTACTACGTTTGGACGCTTGGGGCAAGGAGCACCGGTCAACGCTTCC 849
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 228 -----SerThrAlaSerSerIeuAspTyrlTrpGIyGlnGIyThrIeuValThrValSer 245
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 850 TCAGGATCCGAACAAAACTGATCAGCGAAGAGATCGAACCATCACCATCACCAT 906
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 246 Ser-----HisHisHisHisHisHisHis 252
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
```

Search completed: February 18, 2005, 08:54:37  
Job time : 209 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: February 18, 2005, 08:45:58 ; Search time 82 Seconds

(without alignments)  
1898,440 Million cell updates/sec

Title: US-09-194-164-14

Perfect score: 1582  
Sequence: 1 EFMKKTALVALAGPATV.....GSEOKLISEEDLNHHHKKL 304Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03: \*  
1: uniprot\_prot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	688	43.5	262	2	Q65Z11 mus musculi
2	555	35.1	236	2	Q6P5S8
3	548	34.6	236	2	Q6P1L8
4	547.5	34.6	235	2	Q6GMV9
5	544.5	34.4	235	2	Q6P1F2
6	530	33.5	109	2	Q9UL78
7	526	33.2	129	1	KV3L_HUMAN
8	523	33.1	109	1	KV3B_HUMAN
9	520	32.9	129	1	KV3M_HUMAN
10	515.5	32.6	613	2	Q8WUK1
11	510	32.2	109	1	KV3D_HUMAN
12	506	32.0	109	1	KV3E_HUMAN
13	506	32.0	240	2	Q65ZC9
14	498.5	31.5	122	1	HV3G_HUMAN
15	497	31.4	109	2	Q9UL86
16	493	31.0	116	2	Q9UL93
17	491	31.0	109	1	KV3G_HUMAN
18	486.5	30.8	147	2	Q9Y5O9
19	484	30.6	108	1	KV3A_HUMAN
20	480	30.3	113	2	Q9UL90
21	478	30.2	478	2	Q6P181
22	475	30.0	472	2	Q6N089
23	473.5	29.9	573	2	Q8WU38
24	470	29.7	100	1	KV3C_HUMAN
25	468.5	29.6	235	2	Q6GMW0
26	467.5	29.6	606	2	Q6GMV2
27	466	29.5	236	2	Q6P1H7
28	463.5	29.3	122	1	HV3H_HUMAN
29	463.5	29.3	544	2	Q6P195
30	463	29.3	121	1	HV3J_HUMAN
31	458.5	29.0	122	2	Q9UL84

32	457	28.9	597	2	Q96BB9	Q96BB9 homo sapien
33	455	28.8	119	1	HV3I_HUMAN	P01770 homo sapien
34	455	28.8	121	2	Q9UL71	Q9UL71 homo sapien
35	454	28.7	109	2	Q9UL85	Q9UL85 homo sapien
36	451	28.5	493	2	Q8NCL6	Q8NCL6 homo sapien
37	449.5	28.4	128	1	KV3K_HUMAN	P06311 homo sapien
38	449	28.4	109	1	KV3F_HUMAN	P01624 homo sapien
39	449	28.4	493	2	Q6BCN4	Q6BCN4 homo sapien
40	448.5	28.4	126	1	HV3K_HUMAN	P01772 homo sapien
41	448	28.3	129	1	KV3H_HUMAN	P04207 homo sapien
42	445	28.1	464	2	Q6MZU6	Q6MZU6 homo sapien
43	444	28.1	470	2	Q6P1A4	Q6P1A4 homo sapien
44	443	28.0	519	2	Q6N092	Q6N092 homo sapien
45	442	27.9	482	2	Q7Z351	Q7Z351 homo sapien

## ALIGNMENTS

RESULT 1									
ID	Q65Z11	PRELIMINARY;	PRT;	262	AA.				
AC	Q65Z11;								
DT	25-OCT-2004 (TREMBLrel. 28, Created)								
DT	25-OCT-2004 (TREMBLrel. 28, Last sequence update)								
DT	25-OCT-2004 (TREMBLrel. 28, Last annotation update)								
DE	Anti-HIV-1 reverse transcriptase single-chain variable.								
OS	Mus musculus (Mouse).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
CC	Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.								
OX	NCBI_Taxid=10090;								
RN	(1)								
RP	SEQUENCE FROM N.A.								
RC	TISSUE=Hydridoma;								
RX	MEDLINE=96211469; PubMed=8648670;								
RA	Shaeen F., Duan L., Zhu M., Bagasara O., Pomerantz R.J.;								
RT	"Targeting human immunodeficiency virus type 1 reverse transcriptase								
RT	by intracellular expression of single-chain variable fragments to								
RT	inhibit early stages of the viral life cycle."								
RL	J. Virol. 70:3392-3400(1996).								
DR	EMBL; U48716; AB64342.1; -								
DR	GO: GO:0003964; F:RNA-directed DNA polymerase activity; IEA.								
DR	InterPro; IPR003599; IG.								
DR	InterPro; IPR007110; IG-1-like.								
DR	InterPro; IPR003598; IG_C2.								
DR	InterPro; IPR003596; IG_V.								
DR	Pfam; PF00047; IG_2.								
DR	SMART; SM00409; IG_2.								
DR	SMART; SM00408; IGC2; 2.								
DR	SMART; SM00406; IGV; 2.								
DR	PROSITE; PS50835; IG LIKE; 2.								
KW	RNA-directed DNA polymerase.								
SO	SEQUENCE 262 AA; 27842 MW; 7DF20138E53865B4 CRC64;								
Query Match									
Beet Local Similarity 43.5%; Score 688; DB 2; Length 262;									
Matches 142; Conservative 44; Mismatches 60; Indels 30; Gaps 6;									
QY	24	DIVLTQSGTSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLLYGASTRATGMP	83						
DB	2	DIIMTQSPATLSVTPGDRVSLSCRASQSI-SDFLMYQKSHESRPLLIKVASQSISSGIP	60						
QY	84	DRFSGSGSGTDTLTLSLPEPEFAVYCCQYGGSSPQTPQITFGGCTKVEIKRTVAAPSV	143						
DB	61	SRFSGSGSGDPTLSINSVEPEDEVYVCQNHSPF---LTFGAGTKLELRADAPTV	116						
QY	144	S-----GGGGSGGSGGGGSGG-----SQVQLVESGGGVQGRSLRLSCAASGPPF	188						
DB	117	SLPPSSKLGPGGSGGSGGSGGSGSELGRSSVQLQESGPSIVKPSQTSLTLCVVGDSI	176						
QY	189	RSFAMHWROALGKLEWVAVISYDSTKYVADSVKGRFTTSDRSKNTVYLKMSLRAT	248						
DB	177	TSGYNNWIRKPKGNKLDYMGVITNYSGDT--YNNPSLKSHISTADTSKQYVQLNLSVTTE	235						

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QY 249 DRAVYICARDQSLGIDYHRYGLDWGKGTTVSS 284
DB 236 DAATYCGGGLR-----MDYWGQGTSTVSS 262

RESULT 2
ID Q6P58 PRELIMINARY, PRT, 236 AA.
AC Q6P58;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxId=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Glandular pool- thyroid;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Paley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Glandular pool- thyroid;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR HSSP; P01837; IKCU.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG_2.
DR SMART; SM00407; IGcl; 1.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG_2.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25773 MW; 953E37BEB4FF5F27 CRC64;

Query Match 35.1%; Score 555; DB 2; Length 236;
Best Local Similarity 57.8%; Pred. No. 2e-34;
Matches 126; Conservative 18; Mismatches 48; Indels 26; Gaps 6;

QY 24 DIVTQSPGTLSPGERATLSCRAQSVSSSYLAWYQKPGQAPRLIYGASTRATGMP 83
DB 21 EIVTQSPGTLSPGERATLSCRAQSVSSSYLAWYQKPGQAPRLIYGASTRATGMP 80
QY 84 DRFGSGSGGTPTLTISLPEDPRAVYICQOYGSPQTPQTGGGKVEIKRTVAAPSV 143
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DB 81 DRFGSGSGGTPTLTITLPEDPFAVYICQOYGTG---PSLTFGGGTVEIKRTVAAPSV 137
QY 144 SGGGSGGGGSGGGGSGGVVQPGSRILSLSCAASGPPRRPAMW-VQALGK 202
DB 138 -----RFPSPDEQLSGTASV-----CLNNFYREAKVQKVNALQS 178

QY 203 GLEWAVISYDGTTRYVADSVKGRFTISR-DTSKNTRY 239
DB 179 GNSQSVTEQDSKDSSTY--SLSTLTLSKADYEKKHY 214

RESULT 3
ID Q6P18 PRELIMINARY, PRT, 236 AA.
AC Q6P18;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxId=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Paley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR HSSP; P01837; IKCU.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG_2.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25834 MW; 66479A9E77A3C0053 CRC64;

Query Match 34.6%; Score 548; DB 2; Length 236;
Best Local Similarity 58.8%; Pred. No. 6.8e-34;
Matches 127; Conservative 14; Mismatches 49; Indels 26; Gaps 6;

QY 26 VLTQSPGTLSPGERATLSCRAQSVSSSYLAWYQKPGQAPRLIYGASTRATGMPDR 85
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Db      23 VLTGPGTILSLSPGERATILSCRASQSLSSYLAMVQKQAPRLITVSSRATGTPR 82
Qy      86 FSGSGSGTDFLTLLTIRLEPEDFAVYVYCOQYSSPOTPOITFGGCTKVEIKRTVAAPSV 145
Db      83 FSGSGSGTDFLTLLTIRLEPEDFAVYVYCOQYSSPOTPOITFGGCTKVEIKRTVAAPSV 137
Qy      146 GGGSGGGSGGGGSGQVQVYVSGGGVYVQPGSLRLSCAASGPPRSPFAMHW-VKQALGKL 204
Db      138 -----FIPPPSDEQLKSGTASV-----CLNNFYPREAKVQMKVDNALQSN 180
Qy      205 EMVAIVSYDGTSTKYVADSVKGRFTISR-DTSKNYV 239
Db      181 SOESVTEBDSKDY--SLSTLTLSKADYEKKVY 214

RESULT 4
OG6MV9 PRELIMINARY; PRT; 235 AA.
AC 06GMV9;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Cavalet T.L., Scheetz T.E.,
RA Brownstein M.J., Ushin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalske U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073793; AAH73793.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; Cl-seel; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25646 MW; DF32B580BAD19E4B CRC64;

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Query Match 34.6%; Score 547.5; DB 2; Length 235;
Best Local Similarity 57.8%; Pred. No. 7, 4e-34;
Matches 126; Conservative 15; Mismatches 50; Indels 27; Gaps 6;

Qy      24 DIVLQSPPTLSLSPGERATILSCRASQSSSYLAMYQKQAPRLITVSSRATGTPR 83
Db      21 EIVLQSPPTLSLSPGERATILSCRASQSSSYLAMYQKQAPRLITVSSRATGTPR 80
Qy      84 DRFGSGSGTDFLTLLTIRLEPEDFAVYVYCOQYSSPOTPOITFGGCTKVEIKRTVAAPSV 143
Db      81 DRFGSGSGTDFLTLLTIRLESEDFAVYVYCOQYSSPOTPOITFGGCTKVEIKRTVAAPSV 136
Qy      144 SGGSGSGGGGSGGGGSGQVQVYVSGGGVYVQPGSLRLSCAASGPPRSPFAMHW-VKQALGK 202
Db      137 -----FIPPPSDEQLKSGTASV-----CLNNFYPREAKVQMKVDNALQSN 177
Qy      203 GLEWVAIVSYDGTSTKYVADSVKGRFTISR-DTSKNYV 239
Db      178 GNSQSVTEBDSKDY--SLSTLTLSKADYEKKVY 213

RESULT 5
OG6VF2 PRELIMINARY; PRT; 235 AA.
AC 06VF2;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Cavalet T.L., Scheetz T.E.,
RA Brownstein M.J., Ushin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalske U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016380; AAH16380.1; -.
DR HSSP; P01837; 1KCU.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; Cl-seel; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.

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Db      21 EIVLTQSPGTLSTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLILYGASTRATGIP 80
Oy      84 DRFGSGSGTDTLTITSLRLEPPDPAVYVYCOQYGSSPQTPIFGGATKVEIKR 136
Db      81 DRFGSGSGTDTLTITSLRLEPPDPAVYVYCOQYGSSPQTPIFGGATKVEIKR 129

RESULT 8
KV3B_HUMAN
ID   KV3B_HUMAN          STANDARD;          PRT;          109 AA.
AC   P01620;
DT   21-JUL-1986 (Rel. 01, Created)
DI   21-JUL-1986 (Rel. 01, Last sequence update)
DE   05-JUL-2004 (Rel. 44, Last annotation update)
DR   Ig kappa chain V-II region SIE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX   NCBI_TaxID=9606;

[1]
SEQUENCE
RX   MEDLINE=82046598; PubMed=6794615;
RA   Andrews D.W., Capra J.D.;
RT   "Amino acid sequence of the variable regions of light chains from two
RT   idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT   group."
RL   Biochemistry 20:5816-5822(1981).
CC   -1- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC   globulin activity.
DR   PIR: A01892; KAHUSI.
DR   HSP; P01625; IIVE.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; Ig_1.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS00835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region.
FT   DISULFID 23 89
FT   NON TER 109 109
SQ   SEQUENCE 109 AA; 11775 MW; 7689C3BCD646FFB4 CRC64;

Query Match      33.1%; Score 523; DB 1; Length 109;
Best Local Similarity 90.3%; Pred. No. 2, 2e-32;
Matches 102; Conservative 6; Mismatches 1; Indels 4; Gaps 1;

Oy      24 DIVLTQSPGTLSTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLILYGASTRATGIP 83
Db      1 EIVLTQSPGTLSTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLILYGASTRATGIP 60

Oy      84 DRFGSGSGTDTLTITSLRLEPPDPAVYVYCOQYGSSPQTPIFGGATKVEIKR 136
Db      61 DRFGSGSGTDTLTITSLRLEPPDPAVYVYCOQYGSSPQTPIFGGATKVEIKR 109

RESULT 9
KV3M_HUMAN
ID   KV3M_HUMAN          STANDARD;          PRT;          129 AA.
AC   P18136;
DT   01-NOV-1990 (Rel. 16, Created)
DI   01-NOV-1990 (Rel. 16, Last sequence update)
DE   15-JUN-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-III region HIC precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX   NCBI_TaxID=9606;

[1]
SEQUENCE FROM N.A.
RX   MEDLINE=86171307; PubMed=3127527;
RA   Kippes T.J., Tomhave E., Chen P.P., Carson D.A.;

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RT      "Autoantibody-associated kappa light chain variable region gene
RT      expressed in chronic lymphocytic leukemia with little or no somatic
RT      mutation. Implications for etiology and immunotherapy."
RL   J. Exp. Med. 167:840-852(1988).
CC   -1- DISBASE: The protein is one of the surface immunoglobulin M
CC   autoantibodies expressed in patients with chronic lymphocytic
CC   leukemia.
DR   PIR; P10021; KAHUHI.
DR   HSP; P01625; IIEQ.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; Ig_1.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS00835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL 1 20
FT   CHAIN 21 129
FT   DOMAIN 21 129
FT   DOMAIN 21 43
FT   DOMAIN 44 55
FT   DOMAIN 56 70
FT   DOMAIN 71 77
FT   DOMAIN 78 109
FT   DOMAIN 110 118
FT   DOMAIN 119 129
FT   DISULFID 43 109
FT   NON TER 129 129
SQ   SEQUENCE 129 AA; 14070 MW; 7395528EA2BB74D6 CRC64;

Query Match      32.9%; Score 520; DB 1; Length 129;
Best Local Similarity 91.2%; Pred. No. 4, 6e-32;
Matches 103; Conservative 3; Mismatches 3; Indels 4; Gaps 1;

Oy      24 DIVLTQSPGTLSTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLILYGASTRATGIP 83
Db      21 EIVLTQSPGTLSTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLILYGASTRATGIP 80

Oy      84 DRFGSGSGTDTLTITSLRLEPPDPAVYVYCOQYGSSPQTPIFGGATKVEIKR 136
Db      81 DRFGSGSGTDTLTITSLRLEPPDPAVYVYCOQYGSSPQTPIFGGATKVEIKR 129

RESULT 10
O8WUK1
ID   O8WUK1              PRELIMINARY;          PRT;          613 AA.
AC   O8WUK1;
DT   01-MAR-2002 (TREMBLrel. 20, Created)
DI   01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DE   01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DR   IGHM protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX   NCBI_TaxID=9606;

[1]
SEQUENCE FROM N.A.
RX   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Berger J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Mariani K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein W.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullah S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huijck S.W.,
RA   Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzyzanski M.I., Skalske U., Smalins D.E., Scherch A., Schein J.E.,  
RA Jones S.J., Maitra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RA Strauberg R.,  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL, BC020240, AAH20240.1, -  
DR PIR, F36005, F36005.  
DR PIR, G36005, G36005.  
DR PIR, PH1642, PH1642.  
DR PIR, PH1643, PH1643.  
DR PIR, PH1645, PH1645.  
DR PIR, PH1646, PH1646.  
DR PIR, PL0098, PL0098.  
DR PIR, PL0120, PL0120.  
DR PIR, S15590, S15590.  
DR PIR, S31116, S31116.  
DR PIR, S31119, S31119.  
DR PIR, S70442, S70442.  
DR HSSP, P01861, IADQ.  
DR Pfam, PF07654, Cl-sef, 4.  
DR SMART, SM00406, IGV, 1.  
DR PROSITE, PS00835, IG\_LIKE, 5.  
DR PROSITE, PS00290, IG\_MEC, UNKNOWN, 3.  
SQ SEQUENCE 613 AA, 67295 MW, 60C7F5950671E315 CRC64;

Query Match 32.6%; Score 515.5; DB 2; Length 613;  
Best Local Similarity 79.5%; Pred. No. 6,2e-31;

Matches 101; Conservative 7; Mismatches 14; Indels 5; Gaps 1;

QY 160 QVQLVESGGGVYQPGSLRLSCAASGFPSPRFAMHWVRQALGKLEWVAISYDSSTKY 219  
DB 20 QVQLVSGGGVYQPGSLRLSCAASGFPSPSGMHWVRQALPKGLEWVAISYDSNKY 79  
QY 220 ADSVGRFTISRDTSKNTYYLKMSRTFDYAVYYCARQSLIGDYDHYGLDVGKGT 279  
DB 80 ADSVGRFTISRDTSKNTYYLKMSRTFDYAVYYCARQSLIGDYDHYGLDVGKGT 134  
QY 280 VTVSSGS 286  
DB 135 VTVSSGS 141

RESULT 11  
KV3D HUMAN STANDARD; PRT; 109 AA.  
AC P01623;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Ig kappa chain V-II region Ti.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OK NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=72188439; PubMed=5027703;  
RA Suter L., Barikol H.U., Matanabe S., Hilschmann N.,  
RT "Rule of antibody structure. The primary structure of a monoclonal  
RT immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein  
RT Ti). IV. The complete amino acid sequence and its significance for the  
RT mechanism of antibody production.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).  
CC -I- MISCELLANEOUS: The C region of this chain has the INV (3) marker.  
CC PIR, A01895; K3HUT1.

DR HSSP, P01625, ILVE.  
DR GO, GO:0005576, C:extracellular; NAS.  
DR GO, GO:0003823, F:antigen binding; NAS.  
DR GO, GO:0006955, P:immune response; NAS.  
DR InterPro, IPR007110, Ig-like.  
DR InterPro, IPR003596, Ig\_v.  
DR Pfam, PF00047, Ig, 1.  
DR SMART, SM00406, IGV, 1.  
DR PROSITE, PS00835, IG\_LIKE, 1.  
KW Bence-Jones protein; Direct protein sequencing;  
KW Immunoglobulin V region.  
FT DISULFID 23 89  
FT NON\_TER 109 109 By similarity.  
SQ SEQUENCE 109 AA, 11788 MW, 8C35058C0C77499C CRC64;

Query Match 32.2%; Score 510; DB 1; Length 109;  
Best Local Similarity 88.5%; Pred. No. 2,2e-31;  
Matches 100; Conservative 6; Mismatches 3; Indels 4; Gaps 1;

QY 24 DIVLTQSPGTLISLSPGERATLSCRASGVSSSYLAWYQKRGQAPRLIYGASTRATGMP 83  
DB 1 EIVLTQSPGTLISLSPGERATLSCRASGVSSNSFLAWYQKRGQAPRLIYVASSRATGIP 60  
QY 84 DRFGSGSGTDPFTLTISRLPEDEPAVYVYCCQYGSSTPQTTPGSGTKVEIKR 136  
DB 61 DRFGSGSGTDPFTLTISRLPEDEPAVYVYCCQYGSSTPQTTPGSGTKVEIKR 109

#### RESULT 12

KV3E HUMAN STANDARD; PRT; 109 AA.  
ID KV3E HUMAN STANDARD; PRT; 109 AA.  
AC P01623;

DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Ig kappa chain V-II region WOL.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OK NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE.  
RX MEDLINE=82046598; PubMed=6794615;

RA Andrews D.W., Capra J.D.;

RT "Amino acid sequence of the variable regions of light chains from two  
RT idioypically cross-reactive human Igm anti-gamma-globulins of the Wa  
RT group.";

RL Biochemistry 20:5816-5822(1981).  
CC -I- MISCELLANEOUS: This chain was isolated from an Igm with anti-gamma

CC globulin activity.

DR PIR, A01896, K3HUTL.

DR HSSP, P01625, ILVE.

DR GO, GO:0005576, C:extracellular; NAS.

DR GO, GO:0003823, F:antigen binding; NAS.

DR GO, GO:0006955, P:immune response; NAS.

DR InterPro, IPR007110, Ig-like.  
DR InterPro, IPR003596, Ig\_v.

DR Pfam, PF00047, IGV, 1.

DR SMART, SM00406, IGV, 1.

DR PROSITE, PS00835, IG\_LIKE, 1.

KW Direct protein sequencing; Immunoglobulin V region.  
FT DISULFID 23 89  
FT NON\_TER 109 109 By similarity.

SQ SEQUENCE 109 AA, 11746 MW, 566C1156B9CBEEB CRC64;

Query Match 32.0%; Score 506; DB 1; Length 109;  
Best Local Similarity 88.5%; Pred. No. 4,4e-31;  
Matches 100; Conservative 4; Mismatches 5; Indels 4; Gaps 1;

QY 24 DIVLTQSPGTLISLSPGERATLSCRASGVSSSYLAWYQKRGQAPRLIYGASTRATGMP 83  
DB 1 EIVLTQSPGTLISLSPGERATLSCRASGVSSSYLAWYQKRGQAPRLIYVASSRATGIP 60

QY 84 DRFGSSGCTPDLTISRLEPDPVYVYCOYSSPQTPIFGGKTKEIKR 136  
 DB 61 DRFGSSGCTPDLTISRLEPDPVYVYCOYSSPQTPIFGGKTKEIKR 109

## RESULT 13

Q652C9 PRELIMINARY; PRT; 240 AA.  
 AC Q652C9;  
 DT 25-OCT-2004 (TREMBLrel. 28, Created)  
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)  
 DE Single-chain Fv (Fragment).  
 GN Name=SCFV;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OC NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C1q/7;  
 RX MEDLINE=9736279; PubMed=9219263;  
 RA Kontermann R.E., Wing M.G., Winter G.;  
 RT "Complement recruitment using bispecific diabodies";  
 RL Nat. Biotechnol. 15:629-631(1997).  
 DR EMBL, Y13056; CAA73499.1; -.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; Ig; 2.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00406; IG; 2.  
 DR PROSITE; PS50835; IG\_LIKE; 2.  
 DR NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 240 AA; 25569 MW; FDCPD3645F64B373 CRC64;

Query Match 32.0%; Score 506; DB 2; Length 240;  
 Best Local Similarity 80.2%; Pred. No. 1.1e-30;  
 Matches 101; Conservative 5; Mismatches 12; Indels 8; Gaps 2;

QY 160 QVQLVSGGCVVQPSRLRLSCAAGFPFRSFMHVRQALGKLEWAVISYDSSTKY 219  
 DB 1 QVQLVSGGCVVQPSRLRLSCAAGFPFRSFMHVRQALGKLEWAVISYDSSTKY 60  
 QY 220 ADSVKGRTISRDTSKNTVYLLKMSLRTEDTAVYVYCARQDSLGDYDHYGADVWGKGT 279  
 DB 61 ADSVKGRTISRDTSKNTVYLLKMSLRTEDTAVYVYCARQDSLGDYDHYGADVWGKGT 112  
 QY 280 VTVSSG 285  
 DB 113 VTVSSG 118

## RESULT 14

Q652C9 PRELIMINARY; PRT; 122 AA.  
 AC Q652C9;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Ig heavy chain V-III region CAM.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OC NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=81013859; PubMed=6774332;  
 RA Lehman D.W., Putnam F.W.;  
 RT "Amino acid sequence of the variable region of a human mu chain:  
 location of a possible JH segment";  
 RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).

CC -1- MISCELLANEOUS: This mu chain was isolated from the plasma of a  
 CC patient with macroglobulinemia.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A02051; M3HUM.  
 DR HSSP; P01772; 2PB4.  
 DR GO; GO:0005576; Centriacellular; NAS.  
 DR GO; GO:0003823; F-antigen binding; NAS.  
 DR GO; GO:0006955; P-immune response; NAS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IG; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR Direct protein sequencing; Immunoglobulin V region;  
 KW Pyrolydione carboxylic acid.  
 FT DOMAIN 1 112  
 FT MOD\_RES 1 1  
 FT NON\_TER 122  
 SQ SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;

## Query Match

Best Local Similarity 74.4%; Pred. No. 1.9e-30;  
 Matches 93; Conservative 15; Mismatches 14; Indels 3; Gaps 1;

QY 160 QVQLVSGGCVVQPSRLRLSCAAGFPFRSFMHVRQALGKLEWAVISYDSSTKY 219  
 DB 1 QVQLVSGGCVVQPSRLRLSCAAGFPFRSFMHVRQALGKLEWAVISYDSSTKY 60  
 QY 220 ADSVKGRTISRDTSKNTVYLLKMSLRTEDTAVYVYCARQDSLGDYDHYGADVWGKGT 279  
 DB 61 ADSVKGRTISRDTSKNTVYLLKMSLRTEDTAVYVYCARQDSLGDYDHYGADVWGKGT 117  
 QY 280 VTVSS 284  
 DB 118 VTVSS 122

## RESULT 15

Q9UL86 PRELIMINARY; PRT; 109 AA.  
 ID Q9UL86;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Myosin-reactive immunoglobulin kappa chain variable region  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OC NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cclin.1998.4531;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus";  
 RT Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL; AF035028; AAD56264.1; -.  
 DR PIR; B30607; B30607.  
 DR PIR; B30601; B30601.  
 DR HSSP; P01625; IER3.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR SMART; SM00406; IG; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DACC83 CRC64;

## Query Match

Best Local Similarity 87.6%; Pred. No. 2.2e-30;  
 Matches 99; Conservative 4; Mismatches 6; Indels 4; Gaps 1;

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Page 8

QY	2	DIVTQSPGKLTSLSPGKRALTSCRASSQSVSSYLAWYQKPGAPRLILYGASTATGMP	83
Db	1	EIVLTQSPGKLTSLSPGKRALTSCRASSQSVSSYLAWYQKPGAPRLILILYGSRRATGTP	60
QY	84	DRSGSSGSGNDPFLITLSRLPEPDPAWYVYCOQVSSPQTLQITPGGKTVEIKR	136
Db	61	DRSGSSGSGNDPFLITLSRLPEPDPAWYVYCOQVSS-----LFTPGPTKVDIKR	109

Search completed: February 18, 2005, 08:57:28  
Job time : 83 secs



CC gene therapy. The human monoclonal antibody (MAb), designated H11,  
 CC specifically recognises cancerous cells. H11 is specific for  
 CC glioblastoma, neuroblastoma, malignant melanoma, breast adenocarcinoma,  
 CC lung adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and  
 CC prostate adenocarcinoma  
 XX  
 SQ Sequence 304 AA;

Query Match 100.0%; Score 1582; DB 2; Length 304;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-102;  
 Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EFMKKTATATAVNALAGFATVAQADIVLTQSPGTLSLSPGERATLSCASQSVSSSYLAWY 60  
 DB 1 EFMKKTATATAVNALAGFATVAQADIVLTQSPGTLSLSPGERATLSCASQSVSSSYLAWY 60  
 QY 61 QOKRGAAPRLLIYGASTRATGMPDRFSGSGSGTDFTLTISRLEPEDPAVYYCQYGSPPQ 120  
 DB 61 QOKRGAAPRLLIYGASTRATGMPDRFSGSGSGTDFTLTISRLEPEDPAVYYCQYGSPPQ 120  
 QY 121 TPQITFGGTVKVEIKRTVAAPSVGGSGSGSGGVQVLESQGVVQPGRLRLS 180  
 DB 121 TPQITFGGTVKVEIKRTVAAPSVGGSGSGSGGVQVLESQGVVQPGRLRLS 180  
 QY 181 CAASGPPFRSFAHMYVQALGKLEWYAVISYDSTKYVADSVKGRFTISRDTSKNTYYL 240  
 DB 181 CAASGPPFRSFAHMYVQALGKLEWYAVISYDSTKYVADSVKGRFTISRDTSKNTYYL 240  
 QY 241 KMSLRTEDTAVYYCARDQSLGDYHYGLDVGKGTITVSSGSQKLISEEDLNHHH 300  
 DB 241 KMSLRTEDTAVYYCARDQSLGDYHYGLDVGKGTITVSSGSQKLISEEDLNHHH 300  
 QY 301 HHKL 304  
 DB 301 HHKL 304

## RESULT 2

AAE00947  
 ID AAE00947 standard; protein; 304 AA.

XX AAE00947;  
 DE 04-JUL-2001 (first entry)

XX Human monoclonal antibody H11-single chain variable region (scFv) #1.

XX Human; monoclonal antibody; Mab; H11; single chain variable region; scFv;  
 KW neoplastic disease; melanoma; immunoglobulin IgM; gene therapy; lymphoma;  
 KW carcinoma; breast; lung; gastric; prostate; ovary; colon; lung; vaccine;  
 KW neuroblastoma; soft tissue sarcoma; prostatic adenocarcinoma; cytostatic;  
 KW C-antigen; chronic leukemia; glioma.

OS Homo sapiens.

XX Key Location/Qualifiers  
 XX Region 144..158  
 XX /label= linker  
 XX Misc-difference 302..303  
 XX /note="Encoded by CATTAGTGAAG"

PN US6207153-B1.

PD 27-MAR-2001.

PP 22-MAY-1997; 97US-00862124.

PR 22-MAY-1996; 96US-00657449.

PA (VIVE-) VIVENTIA BIOTECH INC.

PI Dan MD, Maizi PK, Kaplan HA;

DR WPI; 2001-289584/30.  
 DR N-PSDB; AAD04537.

XX Composition comprising antigen binding fragments of an antibody that  
 PT recognizes an antigen on neoplastic cells but not on normal cells for use  
 PT in diagnosis, imaging and treatment of carcinomas.  
 XX  
 PS Claim 1; Col 63-66; 56pp; English.

XX The present sequence is human monoclonal antibody (Mab), H11-single chain  
 CC variable region (scFv). The H11 light chain variable region is linked to  
 CC the heavy chain variable region through a (SGGGG)3 linker to form  
 CC monomers. The invention relates to human monoclonal antibody (Mab) H11,  
 CC H11-(scFv) single chain variable (V) region fragment and their  
 CC corresponding DNA molecules. H11 antibody is an immunoglobulin of IgM  
 CC subclass which is specific to C-antigen found specifically on neoplastic  
 CC cells and not on normal cells. H11 is an antibody obtained from the  
 CC fusion of peripheral blood lymphocytes of a 64 year old male with a low  
 CC grade glioma and fused to a human myeloma cell line to produce a  
 CC hybridoma designated NBGM1/H11. A pharmaceutical composition comprising  
 CC H11 and its derivatives are useful in the diagnosis, imaging and  
 CC treatment of neoplastic disease, particularly, melanoma, breast  
 CC carcinoma, lung carcinoma, ovarian carcinoma, colon carcinoma, gastric  
 CC carcinoma, prostate carcinoma, lymphoma carcinoma, neuroblastoma, glioma,  
 CC soft tissue sarcoma, small cell lung carcinoma, prostatic adenocarcinoma,  
 CC B and T cell lymphomas and chronic leukemias. H11 DNA is also used in  
 CC vaccines and gene therapy  
 XX

SQ Sequence 304 AA;

Query Match 100.0%; Score 1582; DB 4; Length 304;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-102;  
 Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EFMKKTATATAVNALAGFATVAQADIVLTQSPGTLSLSPGERATLSCASQSVSSSYLAWY 60  
 DB 1 EFMKKTATATAVNALAGFATVAQADIVLTQSPGTLSLSPGERATLSCASQSVSSSYLAWY 60  
 QY 61 QOKRGAAPRLLIYGASTRATGMPDRFSGSGSGTDFTLTISRLEPEDPAVYYCQYGSPPQ 120  
 DB 61 QOKRGAAPRLLIYGASTRATGMPDRFSGSGSGTDFTLTISRLEPEDPAVYYCQYGSPPQ 120  
 QY 121 TPQITFGGTVKVEIKRTVAAPSVGGSGSGSGGVQVLESQGVVQPGRLRLS 180  
 DB 121 TPQITFGGTVKVEIKRTVAAPSVGGSGSGSGGVQVLESQGVVQPGRLRLS 180  
 QY 181 CAASGPPFRSFAHMYVQALGKLEWYAVISYDSTKYVADSVKGRFTISRDTSKNTYYL 240  
 DB 181 CAASGPPFRSFAHMYVQALGKLEWYAVISYDSTKYVADSVKGRFTISRDTSKNTYYL 240  
 QY 241 KMSLRTEDTAVYYCARDQSLGDYHYGLDVGKGTITVSSGSQKLISEEDLNHHH 300  
 DB 241 KMSLRTEDTAVYYCARDQSLGDYHYGLDVGKGTITVSSGSQKLISEEDLNHHH 300  
 QY 301 HHKL 304  
 DB 301 HHKL 304

## RESULT 3

ABU10486  
 ID ABU10486 standard; protein; 304 AA.

XX ABU10486;

DT 07-AUG-2003 (first entry)

DE C-antigen antibody H11 single chain variable region fragment #1.

XX Human; antibody; H11; single chain variable region; gene therapy; scFv;  
 KW neoplasia; tumour; recurrence risk; C-antigen; melanoma; neuroblastoma;  
 KW glioma; soft tissue sarcoma; small cell lung carcinoma; brain cancer;  
 KW C-antigen specific antibody; alpha1; cancer; vaccine.

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XX OS Homo sapiens.
XX OS Synthetic.
XX PH Key
XX FT Misc-difference 302. .303
XX FT /note="Encoded by CATTAGTGAAG"
XX PN US2003021779-A1.
XX PD 30-JAN-2003.
XX PP 13-FEB-2001; 2001US-00782397.
XX PR 22-MAY-1996; 96US-00657449.
XX PR 22-MAY-1997; 97US-00862124.
XX PA (DANN/) DAN M D.
XX PA (MATT/) MATTI P K.
XX PA (KAPL/) KAPLAN H A.
XX PI Dan MD, Maiti PK, Kaplan HA;
XX DR WPI: 2003-456278/43.
XX DR N-PsDB: ACA62168, ACA62169.
XX PT Novel antigen binding fragment of monoclonal antibody specific for
XX PT antigen detected on neoplastic cells, useful for diagnosing or treating
XX PT cancer, for manufacturing novel reagents and as diagnostic and imaging
XX PT reagent.
XX PS Claim 5; Page 34; 62pp; English.
XX CC The invention relates to a polypeptide which is an antigen binding
XX CC fragment of a monoclonal antibody specific for an antigen detected on
XX CC neoplastic cells. The antigen binding fragment (ABF) is useful for
XX CC treating a patient with a neoplasia. The individual has a clinically
XX CC detectable tumour. The method is useful for palliating the neoplasia. The
XX CC method reduces the risk of recurrence of a clinically detectable tumour.
XX CC The antigen binding fragment is labelled with a therapeutic moiety such
XX CC as radioisotopes or immunomodulators. ABF is useful for detecting C-
XX CC antigen in a sample. The polypeptide is useful for diagnosing, localising
XX CC and/or treating neoplasias, including melanoma, neuroblastoma, glioma,
XX CC soft tissue sarcoma and small cell lung carcinoma. The polypeptide is
XX CC useful for manufacturing novel reagents and for treating and imaging
XX CC brain cancer. ABF is useful as a diagnostic and imaging reagent. The
XX CC composition is useful for eliciting an immune response against neoplasia.
XX CC The polynucleotide is useful in expression systems for the production of
XX CC C-antigen specific antibody, termed H11 or alphaC, as hybridisation
XX CC probes to assay for the presence of alphaC polynucleotide or related
XX CC sequences in a sample, as primers to effect amplification or related
XX CC polynucleotides and in pharmaceutical compositions including vaccines and
XX CC for gene therapy. The polynucleotide is also useful for genetically
XX CC altering cells in vivo, thus treating various types of cancer. The
XX CC polypeptide, polynucleotide and the composition are useful for detecting
XX CC or treating cancer, including therapy of cancer and prophylactic care,
XX CC particularly for decreasing the risk of recurrence. The present sequence
XX CC represents the amino acid sequence of the human C-antigen specific
XX CC antibody H11 single chain variable region fragment, scfv, #1
XX SS Sequence 304 AA:

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Query Match 100.0%; Score 1582; DB 7; Length 304;
Best Local Similarity 100.0%; Pred. No. 3.6e-102;
Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 EEMKKTAAIAVAALGAFATVAQADIVLTQSPGTLSPSPERRATLSGRASQSSSTLAAV 60
DB 1 EEMKKTAAIAVAALGAFATVAQADIVLTQSPGTLSPSPERRATLSGRASQSSSTLAAV 60
QY 61 QOKPGCAPRLLIYGASTRATGMPDRPFGSGSGTDFLTLSRLEPEDFAVYYCQYQSSSPQ 120
DB 61 QOKPGCAPRLLIYGASTRATGMPDRPFGSGSGTDFLTLSRLEPEDFAVYYCQYQSSSPQ 120

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QY 121 TPQITFGGCTKYEIKRTVAAPSVSGGSGSGGSGGSGQVQLVDSGGSVTPPGRSLRLS 180
DB 121 TPQITFGGCTKYEIKRTVAAPSVSGGSGSGGSGGSGGQVQLVDSGGSVTPPGRSLRLS 180
QY 181 CAASGPPRPSFAMHWVROALGKLEWNAVITYDSGSKYYADSVKRFITSRPTSKKTYVL 240
DB 181 CAASGPPRPSFAMHWVROALGKLEWNAVITYDSGSKYYADSVKRFITSRPTSKKTYVL 240
QY 241 KNNSLRTEDTAVYYCARDQSLIGDYPHYGGLDPMWKGITVTYSSGSEQKLISEEDLNHHH 300
DB 241 KNNSLRTEDTAVYYCARDQSLIGDYPHYGGLDPMWKGITVTYSSGSEQKLISEEDLNHHH 300
QY 301 HHKL 304
DB 301 HHKL 304

```

RESULT 4  
AD052296  
ID AD052296 standard; protein; 304 AA.

AC AD052296;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Human antibody H11 scfv protein #1.  
XX  
DE Neoplasm binding fragment; H chain V region; L chain V region; C-antigen;  
KW neoplasia; cancer; vaccine; gene therapy; human;  
KW single chain V region fragment; scfv.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 302. .303  
FT /note="Encoded by CATTAGTGAAG"  
FT US2004091484-A1.  
XX  
PN 13-MAY-2004.  
XX  
PF 29-AUG-2003; 2003US-00651453.  
XX  
PR 22-MAY-1996; 96US-00657449.  
PR 22-MAY-1997; 97US-00862124.  
PR 13-FEB-2001; 2001US-00782397.  
XX  
PA (DANN/) DAN M D.  
PA (MATT/) MATTI P K.  
PA (KAPL/) KAPLAN H A.  
PA (GRAD/) GRAD C.  
PI Dan MD, Maiti PK, Kaplan HA, Grad C;  
XX  
XX WPI: 2004-399136/37.  
DR N-PsDB: AD052295.  
XX  
PT Composition useful for treating neoplasia in patient, comprises antigen  
PT binding fragment of antibody specifically recognizing C-antigen  
PT recognized by antibody comprising H chain V region and L chain V region.  
XX  
XX Claim 5; SEQ ID NO 14; 56pp; English.

The invention relates to a composition comprising an antigen binding fragment of an antibody comprising H chain V region and L chain V region that specifically recognises C-antigen. The invention is useful for treating a patient with a neoplasia. The antigen binding fragment of the antibody is used as diagnostic and imaging reagents. The invention is useful for genetically altering cells in vivo, to treat various types of cancer. It is also useful in vaccine and gene therapy. The present sequence is human antibody H11 single chain V region fragment (scfv).

SQ Sequence 304 AA;  
 Query Match 100.0%; Score 1582; DB 8; Length 304;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-102;  
 Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EFMKKTALIAVVALAGFATVAQADIVLTQSPTLSLSPGERATLSCRAQSOSVSSSYLAWY 60  
 DB 1 EFMKKTALIAVVALAGFATVAQADIVLTQSPTLSLSPGERATLSCRAQSOSVSSSYLAWY 60  
 QY 61 QOKPGQAPRLLIYGASTRATGMPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQOYSSPQ 120  
 DB 61 QOKPGQAPRLLIYGASTRATGMPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQOYSSPQ 120  
 QY 121 TPQITFGGKTVEIKRTVAAPSVSGSGSGSGGVQVLVESGGGVQPGKSLRLS 180  
 DB 121 TPQITFGGKTVEIKRTVAAPSVSGSGSGSGGVQVLVESGGGVQPGKSLRLS 180  
 QY 181 CAASGPPRSPFAMHWVROALGKLEWVAVISYDGS TKRYAASVYKRFITSDTSKNVYL 240  
 DB 181 CAASGPPRSPFAMHWVROALGKLEWVAVISYDGS TKRYAASVYKRFITSDTSKNVYL 240  
 QY 241 KMSLRTEDTAVVYVCARDQSLGDYHYGLDVMGKGTIVVSSGSEOKLISEEDLNHH 300  
 DB 241 KMSLRTEDTAVVYVCARDQSLGDYHYGLDVMGKGTIVVSSGSEOKLISEEDLNHH 300  
 QY 301 HHKL 304  
 DB 301 HHKL 304

RESULT 5  
 AAM40071  
 ID AAM40071 standard; protein; 287 AA.  
 AC AAM40071;  
 XX  
 DT 29-MAY-1998 (first entry)  
 XX  
 DE Human H11-scFv construct dimer forming protein.  
 XX  
 KW H11; monoclonal antibody; Mab; C-antigen; variable region heavy chain;  
 KW V region; H chain; neoplasia; detection; lymphoma; tumour cell; probe;  
 KW primer; vaccine; gene therapy; glioblastoma; neuroblastoma;  
 KW malignant melanoma; adenocarcinoma; small cell lung carcinoma;  
 KW single chain variable region; scFv.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN MO9744461-A2.  
 XX  
 PD 27-NOV-1997.  
 XX  
 PF 22-MAY-1997; 97MO-US008962.  
 XX  
 PR 22-MAY-1996; 96US-00657449.  
 XX  
 PA (NOVO-) NOVOPHARM BIOTECH INC.  
 XX  
 PI Dan MD, Maiti PK, Kaplan HA;  
 XX  
 DR MPI; 1998-018515/02.  
 DR N-PSDB; AAV10119.  
 XX  
 PT Antigen binding fragment from monoclonal antibody, H11 - allows tumour  
 specific detection and treatment of neoplasia.  
 XX  
 PS Claim 5; Page 95-96; 126pp; English.  
 CC This sequence represents a human H11 monoclonal antibody single chain V  
 region fragment (H11-scFv) construct which is capable of forming dimers.  
 CC This construct is used to determine the ability of H11-scFv antibody

CC fragments to bind specifically to the C-antigen on cancer cells. Such  
 CC antigen binding fragments may be used for treating a patient with  
 CC neoplasia. It is especially useful in the detection of lymphomas and  
 CC leukemias where the tumour cells bearing the C antigen are circulating  
 CC in the patients bloodstream. The polynucleotide sequence may be used as a  
 CC primer or a probe and the encoded protein may be used in a vaccine or for  
 CC gene therapy. The human monoclonal antibody (Mab), designated H11,  
 CC specifically recognises cancerous cells. H11 is specific for  
 CC glioblastoma, neuroblastoma, malignant melanoma, breast adenocarcinoma,  
 CC lung adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and  
 CC prostate adenocarcinoma

SQ Sequence 287 AA;  
 Query Match 92.3%; Score 1460.5; DB 2; Length 287;  
 Best Local Similarity 93.8%; Pred. No. 9.7e-94;  
 Matches 285; Conservative 0; Mismatches 2; Indels 17; Gaps 1;

QY 1 EFMKKTALIAVVALAGFATVAQADIVLTQSPTLSLSPGERATLSCRAQSOSVSSSYLAWY 60  
 DB 1 EFMKKTALIAVVALAGFATVAQADIVLTQSPTLSLSPGERATLSCRAQSOSVSSSYLAWY 60  
 QY 61 QOKPGQAPRLLIYGASTRATGMPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQOYSSPQ 120  
 DB 61 QOKPGQAPRLLIYGASTRATGMPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQOYSSPQ 120  
 QY 121 TPQITFGGKTVEIKRTVAAPSVSGSGSGSGGVQVLVESGGGVQPGKSLRLS 180  
 DB 121 TPQITFGGKTVEIKRTVAAPSVSGSGSGSGGVQVLVESGGGVQPGKSLRLS 180  
 QY 181 CAASGPPRSPFAMHWVROALGKLEWVAVISYDGS TKRYAASVYKRFITSDTSKNVYL 240  
 DB 181 CAASGPPRSPFAMHWVROALGKLEWVAVISYDGS TKRYAASVYKRFITSDTSKNVYL 240  
 QY 241 KMSLRTEDTAVVYVCARDQSLGDYHYGLDVMGKGTIVVSSGSEOKLISEEDLNHH 300  
 DB 241 KMSLRTEDTAVVYVCARDQSLGDYHYGLDVMGKGTIVVSSGSEOKLISEEDLNHH 300  
 QY 301 HHKL 304  
 DB 284 HHKL 287

RESULT 6  
 AAE00948  
 ID AAE00948 standard; protein; 287 AA.  
 AC AAE00948;  
 XX  
 DT 04-JUL-2001 (first entry)  
 XX  
 DE Human monoclonal antibody H11-single chain variable region (scFv) #2.  
 XX  
 KW Human; monoclonal antibody; Mab; H11; single chain variable region; scFv;  
 KW neoplastic disease; melanoma; immunoglobulin IGM; gene therapy; lymphoma;  
 KW carcinoma; breast; lung; gastric; prostate; ovary; colon; lung; vaccine;  
 KW neuroblastoma; soft tissue sarcoma; prostatic adenocarcinoma; cytostatic;  
 KW C-antigen; chronic leukaemia; glioma.  
 XX  
 OS Homo sapiens.  
 OS  
 FH Key location/Qualifiers  
 FT Misc-difference 285..286  
 FT /note="Encoded by CATTAGTGAAG"  
 XX  
 PN US6207153-B1.  
 XX  
 PD 27-MAR-2001.  
 XX  
 PF 22-MAY-1997; 97US-00862124.  
 XX  
 PR 22-MAY-1996; 96US-00657449.  
 XX





QY 61 QQRGQAPRLIIYGASTRATGMPDRFSGSGSGTDFTLTISRLPEPDPAVYYCOQYSSPQ 120  
 DB 61 QQRGQAPRLIIYGASTRATGMPDRFSGSGSGTDFTLTISRLPEPDPAVYYCOQYSSPQ 120  
 QY 121 TPQITFGGGTKVEIKRTVAAPSVSGSGSGSGGVQVLVSSGGGVQPGSRLRLS 180  
 DB 121 TPQITFGGGTKVEIKRTVAAPSVSGSGSGSGGVQVLVSSGGGVQPGSRLRLS 163  
 QY 181 CAASGPFPRSFAMHWRQALGKLEWVAVISYDSTKTYADSVKGRFTISRDTSKNTVYL 240  
 DB 164 CAASGPFPRSFAMHWRQALGKLEWVAVISYDSTKTYADSVKGRFTISRDTSKNTVYL 223  
 QY 241 KMSLRTEPDPAVYYCARGDQSLGDYDHYGGLDWKGGTIVVSSGSEQKLISEEDLNHHH 300  
 DB 224 KMSLRTEPDPAVYYCARGDQSLGDYDHYGGLDWKGGTIVVSSGSEQKLISEEDLNHHH 283  
 QY 301 HHKL 304  
 DB 284 HHKL 287

## RESULT 8

AD052299 ID AD052299 standard; protein; 287 AA.

AD052299; AC XX

29-JUL-2004 (first entry) DT XX

Human antibody H11 scFv protein #2. DE XX

Antigen binding fragment; H chain V region; L chain V region; C-antigen; KM XX

neoplasia; cancer; vaccine; gene therapy; human; KM XX

single chain V region fragment; scFv. KW XX

Homo sapiens. OS XX

Key Location/Qualifiers FH XX

Misc-difference 285..286 FT XX

/note="Encoded by CATTAGTGAAG" FT XX

US2004091484-A1. PN XX

13-MAY-2004. PD XX

29-AUG-2003; 2003US-00651453. PF XX

22-MAY-1996; 96US-00657449. PR XX

22-MAY-1997; 97US-00862124. PR XX

13-FEB-2001; 2001US-00782397. PR XX

(DANM/) DAN M D. PA XX

(MAIT/) MAITI P K. PA XX

(KAPL/) KAPLAN H A. PA XX

(GRAD/) GRAD C. PA XX

Dan MD, Maici PK, Kaplan HA, Grad C, PI XX

WPI: 2004-399136/37. DR XX

N-PSDB; AD052298. DR XX

Composition useful for treating neoplasia in patient, comprises antigen binding fragment of antibody specifically recognizing C-antigen PT XX

recognized by antibody comprising H chain V region and L chain V region. PT XX

Claim 5; SEQ ID NO 17; 56bp; English. PS XX

The invention relates to a composition comprising an antigen binding fragment of an antibody comprising H chain V region and L chain V region CC XX

that specifically recognises C-antigen. The invention is useful for CC XX

treating a patient with a neoplasia. The antigen binding fragment of the CC XX

antibody is used as diagnostic and imaging reagents. The invention is CC XX

useful for genetically altering cells in vivo, to treat various types of CC XX

CC cancer. It is also useful in vaccine and gene therapy. The present  
 CC sequence is human antibody H11 single chain V region fragment (scFv).  
 XX

Sequence 287 AA;

Query Match 92.3%; Score 1460.5; DB 8; Length 287;  
 Best Local Similarity 93.8%; Pred. No. 9.7e-94;  
 Matches 285; Conservative 0; Mismatches 2; Indels 17; Gaps 1;

QY 1 EFMKTAIAIAYALAGFATVAQADIVLTQSPGTLISLPEERATLSCRASQSVSSSYLAMY 60  
 DB 1 EFMKTAIAIAYALAGFATVAQADIVLTQSPGTLISLPEERATLSCRASQSVSSSYLAMY 60  
 QY 61 QQRGQAPRLIIYGASTRATGMPDRFSGSGSGTDFTLTISRLPEPDPAVYYCOQYSSPQ 120  
 DB 61 QQRGQAPRLIIYGASTRATGMPDRFSGSGSGTDFTLTISRLPEPDPAVYYCOQYSSPQ 120  
 QY 121 TPQITFGGGTKVEIKRTVAAPSVSGSGSGSGGVQVLVSSGGGVQPGSRLRLS 180  
 DB 121 TPQITFGGGTKVEIKRTVAAPSVSGSGSGSGGVQVLVSSGGGVQPGSRLRLS 163  
 QY 181 CAASGPFPRSFAMHWRQALGKLEWVAVISYDSTKTYADSVKGRFTISRDTSKNTVYL 240  
 DB 164 CAASGPFPRSFAMHWRQALGKLEWVAVISYDSTKTYADSVKGRFTISRDTSKNTVYL 223  
 QY 241 KMSLRTEPDPAVYYCARGDQSLGDYDHYGGLDWKGGTIVVSSGSEQKLISEEDLNHHH 300  
 DB 224 KMSLRTEPDPAVYYCARGDQSLGDYDHYGGLDWKGGTIVVSSGSEQKLISEEDLNHHH 283  
 QY 301 HHKL 304  
 DB 284 HHKL 287

## RESULT 9

AD089103 ID AD089103 standard; protein; 638 AA.

AD089103; AC XX

20-NOV-2003 (first entry) DT XX

Phage display vector amino acid sequence SEQ ID NO:54. DE XX

antigen binding; antibody; specific binding affinity; DE XX

receptor protein tyrosine kinase; RPTK; KW XX

fibroblast growth factor receptor; FGFR; osteopathic; cytostratic; KW XX

ophthalmological; bone disorder; cartilage disorder; skeletal disorder; KW XX

skeletal dysplasia; achondroplasia; thanatophoric dysplasia; KW XX

hypochondroplasia; craniocervical dysplasia; cancer; vision disorder; KW XX

malignant cell proliferative disease; cancer; tumour; vision disorder; KW XX

non-neoplastic angiogenic pathologic condition. KW XX

Synthetic. OS XX

Homo sapiens. OS XX

WO2002102973-A2. PN XX

27-DEC-2002. PD XX

20-JUN-2002; 2002WO-IL000495. PF XX

20-JUN-2001; 2001US-0299187P. PR XX

(PROC-) PROCHON BIOTECH LTD. PA XX

Yayon A, Rom E; PI XX

WPI: 2003-175236/17. DR XX

N-PSDB; AD089102. DR XX

New antibodies which have specific binding affinity for a receptor PT XX

PT protein tyrosine kinase (RPTK) and block constitutive activation of RPTK,  
 CC useful for treating bone and cartilage disorders, or malignant cell  
 PT proliferative diseases.

PS Example 3; Fig 298; 122pp; English.

CC The present invention describes a molecule (1) comprising the antigen  
 CC binding portion of an isolated antibody which has specific binding  
 CC affinity for a receptor protein tyrosine kinase (RPTK), particularly for  
 CC a fibroblast growth factor receptor (FGFR), and which blocks constitutive  
 CC activation of an RPTK. Also described: (1) pharmaceutical compositions  
 CC comprising (1) as an active ingredient and a pharmaceutical carrier,  
 CC excipient, or auxiliary agent; (2) a kit comprising (1), at least one  
 CC reagent for detecting the presence of (1) when bound to the RPTK, and  
 CC instructions for use; (3) a method for treatment of bone and cartilage  
 CC related disorders by administering a composition of (1) to the subject;  
 CC (4) a method for treating or inhibiting a cell proliferative disease or  
 CC disorder by administering the composition of (1); (5) a method for  
 CC screening a molecule comprising the antigen-binding portion of an  
 CC antibody which blocks ligand-dependent activation of RPTK; (6) an  
 CC isolated nucleic acid molecule encoding a V<sub>H</sub>-CDR3 DNA region; (6) an  
 CC CDR3 DNA region; (7) an isolated nucleic acid molecule encoding V<sub>L</sub> region  
 CC and a V<sub>H</sub> region; (8) vectors comprising a nucleic acid molecule of (6) or  
 CC (7); and (9) host cells transformed with the vector. (1) have  
 CC osteopathic, cytostatic and ophthalmological activities, and can be used  
 CC as a RPTK inhibitor. Compositions comprising (1) are useful for treating  
 CC bone and cartilage disorders, including skeletal disorders such as  
 CC skeletal dysplasia (achondroplasia, thanatophoric dysplasia,  
 CC hypochondroplasia, severe achondroplasia with developmental delay and  
 CC acanthosis nigricans dysplasia) or a craniosynostosis disorder (e.g.  
 CC Muenke coronal craniosynostosis or Crouzon syndrome with acanthosis  
 CC nigricans). The composition may also be used for treating or inhibiting  
 CC malignant cell proliferative disease or disorder associated with abnormal  
 CC RPTK activity, including a haematopoietic malignancy (e.g. multiple  
 CC myeloma), solid tumours (e.g. mammary, colon, cervical, bladder,  
 CC colorectal, chondrosarcoma or osteosarcoma), tumour formation, primary  
 CC tumours, tumour progression (particularly progression of transitional  
 CC cell carcinoma or mammary carcinoma), or tumour metastasis, where the  
 CC cell proliferative disorder may be associated with the action of a  
 CC constitutively activated RPTK, or with ligand-dependent activation of  
 CC RPTK. The compositions may further be used for treating  
 CC hyperproliferative diseases and disorders associated with ligand-  
 CC dependent RPTK signaling, such as vision disorders (e.g. neovascular  
 CC glaucoma, macular degeneration and proliferative retinopathy including  
 CC diabetic retinopathy), and non-neoplastic angiogenic pathologic  
 CC conditions (e.g. haemangiomas, angiofibromas and psoriasis). The present  
 CC sequence is given in the exemplification of the present invention.

XX Sequence 638 AA;

Query Match 64.3%; Score 1016.5; DB 6; Length 638;  
 Best Local Similarity 58.0%; Pred. No. 1.8e-62;  
 Matches 225; Conservative 15; Mismatches 35; Indels 113; Gaps 5;

QY 3 MKKTAIAIVNLAGFTVAQADIVLTQSGTSLSGEERATLSCRASQSVSSSYLAWYQO 62  
 DB 1 MKKTAIAIVNLAGFTVAQADIVLTQSGTSLSGEERATLSCRASQSVSSSYLAWYQO 60  
 QY 63 KFGQAPRLIYGASTATGMPDRFSSGSGSTPFTLTISRLEPDPFVYVYCOOVGSSPQRP 122  
 DB 61 KKGQARLLIYGASSTATGVPARFSSGSGSTPFTLTISRLEPDPFVYVYCOOVGSSPQRP 118  
 QY 123 QITFGGTVETIKRTVAAPSV----- 143  
 DB 119 --TFGGTVETIKRTVAAPSVFPPSPDQLKSGTASVCLNNFYPRAKYQWKVDNL 176  
 QY 144 -SG-----GGSGGGGGGGG-- 158  
 DB 177 QGSGQSVTEQDSKOSTYSLSTTLTKADYKHKVYACEVTHQGLSPVTKSPRGRGA 236  
 QY 159 -----SQVQLVESGGGVVQVQPSRLISCAAGSPFRSPAMWVQ 198  
 DB 237 MKGSTIALALPLPLPTPVTKAQVQIVESGGGLVQPGSIRLSGASGFTFSSYAMSWVQ 296

QY 199 ALGKLEWVAIVSYDSTRTYADSVKGRFTISRDTSKNTVYLKMSLRTEEDPAVYICAND 258  
 DB 297 APGKLEWVAISVSGSGSTYADSVKGRFTISRDTSKNTVYLQMSLRTEEDPAVYICAR- 355  
 QY 259 QSLGDPHYGIDVWVGKGTIVTSSGS 286  
 DB 356 ----WGGDFYANDYWGQGLTVTSSAS 379

#### RESULT 10

ADA90139  
 ID ADA90139 standard; protein; 638 AA.  
 AC ADA90139;  
 XX  
 XX 20-NOV-2003 (first entry)  
 DT  
 XX  
 DE Anti-Abeta antibody related amino acid sequence SEQ ID NO:254.

XX antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective;  
 XX neurotropic; antiparkinsonian; gene therapy; amyloidogenesis;  
 XX amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia;  
 XX Alzheimer's disease; motor neuropathy; Down's syndrome;  
 XX Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis;  
 XX Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;  
 XX neuronal disorder; aging.

OS Synthetic.  
 XX Homo sapiens.

XX MO2003070760-A2.

XX 28-AUG-2003.

XX 20-FEB-2003; 2003WQ-BP001759.

XX 20-FEB-2002; 2002EP-00003844.

XX (HOPE) HOFFMANN LA ROCHE & CO AG F.

PA (MORP-) MORPHOSYS AG.

PI Bardot M, Bohrmann B, Brockhaus M, Huber W, Kretschmar T;  
 PI Loehning C, Loetscher H, Nordstedt C, Rothe C;

DR WPI; 2003-663848/62.

XX New antibody molecule capable of specifically recognizing two regions of  
 PT the beta-A4 peptide, useful for diagnosing, preventing or treating  
 PT diseases associated with amyloidogenesis or amyloid-plaque formation  
 PT (e.g. dementia).

PS Disclosure; Page 251-254; 312pp; English.

XX The present invention describes an antibody molecule (1) capable of  
 CC specifically recognising two regions of the beta-A4 peptide/Abeta4. The  
 CC first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-  
 CC Ser-Gly-Tyr ADA89886 or its fragment, and the second region comprises the  
 CC amino acid sequence Val-His-His-Gln-Lys-Ileu-Val-Phe-Phe-Ala-Glu-Asp-Val-  
 CC Gly ADA89887 or its fragment. Also described: (1) a nucleic acid molecule  
 CC encoding (1); (2) a vector comprising the nucleic acid of (1); (3) a host  
 CC cell comprising the vector of (2); (4) preparing (1), comprising  
 CC culturing the host cell of (3) under conditions that allow synthesis of  
 CC (1) and recovering (1) from the culture; (5) a composition comprising (1)  
 CC or an antibody molecule produced by method (4); (6) a kit comprising (1),  
 CC nucleic acid of (1), vector of (2) or host cell of (3); (7) optimising  
 CC (1); (8) testing the resulting Fab optimisation library by panning  
 CC against Abeta4/Abeta4; (9) identifying optimised clones; (10) expressing  
 CC of selected, optimised clones; (11) preparing a pharmaceutical  
 CC composition, comprising optimisation of (1), and formulating the  
 CC optimised antibody/antibody molecule with a carrier; and (12) a  
 CC pharmaceutical composition prepared by method (8). (1) has  
 CC neuroprotective, neurotropic and antiparkinsonian activities, and can be



DB 177 QSGNSQESVTEBDSKDSSTYLSSTLTLSKADYEKKVYACEVTHQGLSPVTKSFNRGA 236  
 QY 159 -----SQVQLVESGGGVGVQPGRSRLSCAASGPPRFAMRWQ 198  
 DB 237 MKQSTIALALPLPTPTKQAQVQLVESGGGLVQPGGSLRLSCAAGFPFSSYAMSWAQ 296  
 QY 199 ALGKLEWVAIVSYDSTKYVADSVKGRFTISRDTSKNTVYKMSLTREDPAVYYCARD 258  
 DB 297 APGKLEWVAISGSGSTYYADSVAGRTTISRDNKNTLYIQNMSLRADPAVYYCAR- 355  
 QY 259 QSLGDDYHYGDLVWGKGTITVSSGS 286  
 DB 356 ----WGDDGFYAMDYWGQGTITVSSAS 379

RESULT 12  
 ADG74355  
 ID ADG74355 standard; protein; 747 AA.  
 XX

AC ADG74355;  
 XX  
 DT 11-MAR-2004 (first entry)  
 XX  
 DE MSPRO light chain variable region protein, SEQ ID NO 92.

antigen binding; receptor protein tyrosine kinase;  
 fibroblast growth factor receptor 3; FGFR3; osteoblastic; cytosolic;  
 neurotrophic; neuroprotective; ophthalmological; antidiabetic; gene therapy;  
 bone; cartilage; cranioynostosis; skeletal dysplasia;  
 cell proliferative disorder; haematopoietic malignancy;  
 hyperproliferative disorder; neurovascular glaucoma;  
 macular degeneration; proliferative retinopathy; diabetic retinopathy;  
 MSPO.

Unidentified.

MO2002102972-A2.

27-DEC-2002.

20-JUN-2002; 2002WO-IL000494.

20-JUN-2001; 2001US-0299187P.

(PROC-) PROCHON BIOTECH LTD.  
 (MORP-) MORPHOSYS AG.

Yayon A, Rom E, Thomassen-Wolf E, Borges E;

WPI; 2003-175235/17.

New antigen binding portion of an antibody having a specific binding  
 affinity for a receptor protein tyrosine kinase, useful for treating bone  
 and cartilage related disorders, cell proliferative or hyperproliferative  
 disorders.

Claim 42; SEQ ID NO 92; 122pp; English.

The invention relates to a novel molecule comprising the antigen binding  
 portion of an isolated antibody having a specific binding affinity for a  
 receptor protein tyrosine kinase, and which blocks constitutive  
 activation of a receptor protein tyrosine kinase, such as fibroblast  
 growth factor receptor 3 (FGFR3). The novel molecules of the invention  
 have the following activities: osteopathic, cytosolic, neurotrophic,  
 neuroprotective, ophthalmological, and antidiabetic. The nucleic acids  
 encoding the novel molecules of the invention can be used in gene therapy  
 to treat disorders. The molecule and nucleic acid molecules are useful  
 for treating bone and cartilage related disorders such as  
 cranioynostosis (e.g. Muenke coronal cranioynostosis or Crouzon  
 syndrome with acanthosis nigricans), or skeletal dysplasia (e.g.  
 achondroplasia, thanatophoric dysplasia (TD), hypochondroplasia, severe  
 dysplasia), cell proliferative disorders, haematopoietic malignancy (e.g.

CC multiple myeloma), hyperproliferative disorders, neurovascular glaucoma,  
 CC macular degeneration or proliferative retinopathy including diabetic  
 CC retinopathy. This sequence represents an MSPRO antibody light chain  
 CC variable region peptide relating to the invention.

Sequence 747 AA;

Query Match 64.3%; Score 1016.5; DB 7; Length 747;  
 Best Local Similarity 58.0%; Pred. No. 2.2e-62;  
 Matches 225; Conservative 15; Mismatches 35; Indels 113; Gaps 5;

QY 3 MKKTAIAVALAGPATVQAQDIYVLTQSPGTSLSPEERATLSCRAQSQSSSYLAWQ 62  
 DB 110 MKKTAIAVALAGPATVQAQDIYVLTQSPATLSLPEERATLSCRAQSQSSSYLAWQ 169  
 QY 63 KPGQAPRLIIVAGSTRATGMPDRFSGSGSDTFTLTISRLEPEDPAVYYCQOYGSPPQTP 122  
 DB 170 KPGQAPRLIIVAGSTRATGMPDRFSGSGSDTFTLTISRLEPEDPAVYYCQOYHTTTP-- 227  
 QY 123 QITFGGQTKVEIKRTVAAPSV----- 143  
 DB 228 --TFGQGTVEIKRTVAAPSVFIPPPSDQLKSGTASVCLINFPYRAKYQWKVDNAL 285  
 QY 144 --SG-----GGSGSGSGSGSG-- 158  
 DB 286 QSGNSQESVTEBDSKDSSTYLSSTLTLSKADYEKKVYACEVTHQGLSPVTKSFNRGA 345  
 QY 159 -----SQVQLVESGGGVGVQPGRSRLSCAASGPPRFAMRWQ 198  
 DB 346 MKQSTIALALPLPTPTKQAQVQLVESGGGLVQPGGSLRLSCAAGFPFSSYAMSWAQ 405  
 QY 199 ALGKLEWVAIVSYDSTKYVADSVKGRFTISRDTSKNTVYKMSLTREDPAVYYCARD 258  
 DB 406 APGKLEWVAISGSGSTYYADSVAGRTTISRDNKNTLYIQNMSLRADPAVYYCAR- 464  
 QY 259 QSLGDDYHYGDLVWGKGTITVSSGS 286  
 DB 465 ----WGDDGFYAMDYWGQGTITVSSAS 488

RESULT 13

AAV44994  
 ID AAV44994 standard; protein; 523 AA.

AAV44994;

DT 23-MAY-2000 (first entry)

DE HD706CFV-CH1-GM-CSF chain.

HD70; single-chain variable fragment; scFv; 17-1A antigen; human; EPCAM;  
 KW epithelial cell adhesion molecule; inflammatory cytokine; GM-CSF;  
 KW granulocyte/macrophage colony stimulating factor; heteromultimer;  
 KW CHI-domain; multifunctional compound; heavy chain constant domain;  
 KW immunoglobulin; cytosolic; immunostimulatory; anti-leukemia; diagnosis;  
 KW antiproliferative; prevention; treatment; malignant; haematopoietic cell;  
 KW lymphoma; leukaemia; solid tumour; carcinoma; melanoma; sarcoma.

Homo sapiens.

MO200006605-A2.

10-FEB-2000.

28-JUL-1999; 99WO-EP005416.

28-JUL-1998; 98EP-00114082.

(MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.

Kuifer P, Dreier T, Baerle PA, Borchert K, Zettl F;

WPI; 2000-195265/17.

DR N-PSDB; AAZ50587.  
 XX  
 PT New multifunctional compounds useful for preventing and/or treating  
 PT malignant cell growth and for detection and diagnosis.  
 XX  
 PS Example 10; Fig 55A; 166pp; English.  
 XX  
 CC The patent discloses heteromimibodies which are multifunctional compounds  
 CC producible in a mammalian host cell as a secretable and fully functional  
 CC heterodimer of two polypeptide chains, where one of the polypeptide  
 CC chains comprises, a CH1-domain (constant domain of an immunoglobulin  
 CC heavy chain) and the other chain comprises CL-domain (constant domain of  
 CC an immunoglobulin light chain). The polypeptide chains further comprise,  
 CC fused to the constant domains at least two (poly)peptides having  
 CC different receptor or ligand functions, where further at least two of the  
 CC different (poly)peptides lack an intrinsic affinity for one another and  
 CC are linked via the constant domains. The heteromimibodies have  
 CC cytostatic, immunostimulatory, antileukaemia and antiproliferative  
 CC activities. These compounds can be used for diagnosing, preventing and  
 CC treating malignant cell growth related to malignancies of haematopoietic  
 CC cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,  
 CC melanomas and sarcomas. The present sequence is the left chain of a  
 CC heteromimibody comprising HD70 single-chain Fv (scFv) Fragment N-  
 CC terminally linked to human CH1 domain which bears at its C-terminus the  
 CC human inflammatory cytokine granulocyte/macrophage colony stimulating  
 CC factor (GM-CSF), plus a hexahistidine sequence for ease of purification.  
 CC HD70 scFv specifically recognises the human epithelial cell adhesion  
 CC molecule (EPCAM) also called 17-1A antigen  
 XX  
 SQ Sequence 523 AA;  
 Query Match 62.3%; Score 986; DB 3; Length 523;  
 Best Local Similarity 69.2%; Pred. No. 1.9e-60;  
 Matches 193; Conservative 32; Mismatches 38; Indels 16; Gaps 4;  
 QY 10 IAVALAGFATVAQADIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAMYQKPGQAPR 69  
 Db 6 ILFLVATATGVHSELQMTQSPSSLSASVGDRTITCRASQSI--SSYLAMWYQKPGQAPR 64  
 QY 70 LLITGASTRATGMPDRFSGSGSGTDFTLTISRLEPEDPAVYVYCOYSSPOTPTITFGG 129  
 Db 65 LLITWASTRESGVDPDRFSGSGSGTNTYLTISLQPEDPAVYVFCQSDSLP---ITFGG 120  
 QY 130 TKVEIKRTVAAPSVVGGGSGGSGGVQVLESQGVVQPGRSIRLSCAASGEPFR 189  
 Db 121 TRLDIQ-----GGGSGGGSGGGSGGVQVLESQGVVQPGRSIRLSCAASGFTFS 171  
 QY 190 SPAMHWRAQALGKLEWNAVIVSYDGSITKYVADSVKGRFTISRDTSKNTVYLKKNLSRTED 249  
 Db 172 SYGMHWRAQAPGKLEWNAVIVSYDGSINKKYADSVKGRFTISRDNSKNTVYLQNNLSRAED 231  
 QY 250 TAVYYCARQDGLDGDY--HYGLDWGKGTITVSSGS 286  
 Db 232 TAVYYCAKDMGSGMRRPYYYGMDVWGQGITVTVSSGT 270  
 RESULT 14  
 AA444995  
 ID AA444995 standard; protein; 524 AA.  
 XX  
 AC AA444995;  
 XX  
 DT 23-MAY-2000 (first entry)  
 XX  
 DE HD70scFv-Ch-interleukin 2.  
 XX  
 KW HD70; single-chain Fv fragment; scFv; antibody; 17-1A antigen; human;  
 KW EPCAM; epithelial cell adhesion molecule; inflammatory cytokine; IL-2;  
 KW interleukin-2; Ch-domain; kappa light chain constant domain;  
 KW heteromimibody; multifunctional compound; immunoglobulin; cytostatic;  
 KW immunostimulatory; antileukaemia; diagnosis; prevention;  
 KW antiproliferative; treatment; malignant; haematopoietic cell; lymphoma;  
 KW leukaemia; solid tumour; carcinoma; melanoma; sarcoma.

XX  
 OS Homo sapiens.  
 XX  
 PN WO200006605-A2.  
 XX  
 PD 10-FEB-2000.  
 XX  
 XX 28-UTL-1999; 99WO-EP005416.  
 XX  
 PR 28-JUL-1998; 98EP-00114082.  
 XX  
 PA (MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.  
 XX  
 PI Kufer P, Dreier T, Baeuerle PA, Borchert K, Zettl P;  
 XX  
 DR WPI; 2000-195265/17.  
 DR N-PSDB; AAZ50588.  
 XX  
 PT New multifunctional compounds useful for preventing and/or treating  
 PT malignant cell growth and for detection and diagnosis.  
 XX  
 PS Example 10; Fig 55B; 166pp; English.  
 XX  
 CC The patent discloses heteromimibodies which are multifunctional compounds  
 CC producible in a mammalian host cell as a secretable and fully functional  
 CC heterodimer of two polypeptide chains, where one of the polypeptide  
 CC chains comprises, a CH1-domain (constant domain of an immunoglobulin  
 CC heavy chain) and the other chain comprises CL-domain (constant domain of  
 CC an immunoglobulin light chain). The polypeptide chains further comprise,  
 CC fused to the constant domains at least two (poly)peptides having  
 CC different receptor or ligand functions, where further at least two of the  
 CC different (poly)peptides lack an intrinsic affinity for one another and  
 CC are linked via the constant domains. The heteromimibodies have  
 CC cytostatic, immunostimulatory, antileukaemia and antiproliferative  
 CC activities. These compounds can be used for diagnosing, preventing and  
 CC treating malignant cell growth related to malignancies of haematopoietic  
 CC cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,  
 CC melanomas and sarcomas. The present sequence is the right chain of a  
 CC heteromimibody comprising HD70 single-chain Fv (scFv) Fragment N-  
 CC terminally linked to human Ck domain (constant domain of immunoglobulin-  
 CC kappa light chain) which bears at its C-terminus the human inflammatory  
 CC cytokine interleukin-2 (IL-2). HD70 scFv specifically recognises the  
 CC human epithelial cell adhesion molecule (EPCAM) also called 17-1A antigen  
 XX  
 SQ Sequence 524 AA;  
 Query Match 62.3%; Score 986; DB 3; Length 524;  
 Best Local Similarity 69.2%; Pred. No. 1.9e-60;  
 Matches 193; Conservative 32; Mismatches 38; Indels 16; Gaps 4;  
 QY 10 IAVALAGFATVAQADIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAMYQKPGQAPR 69  
 Db 6 ILFLVATATGVHSELQMTQSPSSLSASVGDRTITCRASQSI--SSYLAMWYQKPGQAPR 64  
 QY 70 LLITGASTRATGMPDRFSGSGSGTDFTLTISRLEPEDPAVYVYCOYSSPOTPTITFGG 129  
 Db 65 LLITWASTRESGVDPDRFSGSGSGTNTYLTISLQPEDPAVYVFCQSDSLP---ITFGG 120  
 QY 130 TKVEIKRTVAAPSVVGGGSGGSGGVQVLESQGVVQPGRSIRLSCAASGEPFR 189  
 Db 121 TRLDIQ-----GGGSGGGSGGGSGGVQVLESQGVVQPGRSIRLSCAASGFTFS 171  
 QY 190 SPAMHWRAQALGKLEWNAVIVSYDGSITKYVADSVKGRFTISRDTSKNTVYLKKNLSRTED 249  
 Db 172 SYGMHWRAQAPGKLEWNAVIVSYDGSINKKYADSVKGRFTISRDNSKNTVYLQNNLSRAED 231  
 QY 250 TAVYYCARQDGLDGDY--HYGLDWGKGTITVSSGS 286  
 Db 232 TAVYYCAKDMGSGMRRPYYYGMDVWGQGITVTVSSGT 270  
 RESULT 15  
 ABJ38670

ID ABJ38670 standard; protein; 628 AA.  
 AC ABJ38670;  
 DT 26-JUN-2003 (first entry)  
 DE Fab expression vector protein SEQ ID No 96.  
 XX  
 XX Cytostatic; osteopathic; cerebroprotective; dermatological; enzyme;  
 XX antigen binding; receptor protein tyrosine kinase; skeletal dysplasia;  
 XX constitutive activation; craniosynostosis; cell proliferative disorder;  
 XX achondroplasia; thanatophoric dysplasia; acanthosis nigricans dysplasia;  
 XX hypochondroplasia; severe achondroplasia; transitional cell carcinoma;  
 XX Muenke coronal craniosynostosis; Crozin syndrome; acanthosis nigricans;  
 XX tumour progression; osteosarcoma; chondrosarcoma; multiple myeloma;  
 XX mammary carcinoma; fibroblast growth factor receptor 3; FGFR3 protein;  
 XX Fab.  
 OS Homo sapiens.  
 PN WO2002102854-A2.  
 XX  
 XX 27-DEC-2002.  
 PD  
 XX 20-JUN-2002; 2002WO-1B003523.  
 PF  
 XX 20-JUN-2001; 2001US-0299187P.  
 PR  
 XX (MORP-) MORPHOSYS AG.  
 PA (PROC-) PROCHON BIOTECH LTD.  
 PI Thomassen-Wolf E, Borges E, Yaron A, Rom E,  
 XX WPI; 2003-167489/16.  
 DR  
 XX  
 PT New molecules having the antigen-binding portion of antibodies that block  
 PT activation of receptor protein tyrosine kinase, useful for treating or  
 PT inhibiting skeletal dysplasias, craniosynostosis or cell proliferative  
 PT disorders.  
 PS Disclosure; Fig 26B; 103pp; English.  
 XX  
 XX The invention relates to a novel molecule comprising the antigen binding  
 CC portion of an isolated antibody, which has an increased affinity for a  
 CC receptor protein tyrosine kinase and which blocks constitutive activation  
 CC of the receptor protein tyrosine kinase. The methods and compositions of  
 CC the invention are useful for treating or inhibiting a skeletal dysplasia,  
 CC craniosynostosis or a cell proliferative disorder. The skeletal dysplasia  
 CC is achondroplasia, thanatophoric dysplasia, hypochondroplasia, severe  
 CC achondroplasia with developmental delay or acanthosis nigricans  
 CC dysplasia. The craniosynostosis disorder is Muenke coronal  
 CC craniosynostosis or Crozin syndrome with acanthosis nigricans. The cell  
 CC proliferative disorder is tumour progression that is progression of  
 CC transitional cell carcinoma, osteosarcoma, chondrosarcoma, multiple  
 CC myeloma or mammary carcinoma. This sequence represents the protein  
 CC derived from a Fab expression vector relating to the protein tyrosine  
 CC kinase inhibitor of the invention  
 CC  
 SQ Sequence 628 AA;  
 Query Match 61.5%; Score 972.5; DB 6; Length 628;  
 Best Local Similarity 56.9%; Pred. No. 2.1e-59;  
 Matches 215; Conservative 15; Mismatches 35; Indels 113; Gaps 5;  
 QY 13 ALAGFATVQAADIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLI 72  
 DB 1 ALAGFATVQAADIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLI 60  
 QY 73 YASTRTATMPDRPSGSGSGDTFTLTISLPEPDPAVYVCOQYSGSPQPTITFGGTRV 132  
 DB 61 YGASRATGVPARFSGSGSGDTFTLTISLPEPDFAVYVCOOHYTPP---TFGGTRV 116  
 QY 133 EIKRTVAAPSV-----SG----- 145

DB 117 EIKRTVAAPSVFIPPPSDQLKSGTASVYCLINNFYPREAKYQMKVDNALQSGNSQESVT 176  
 QY 146 -----GGSGGGGGGGGG----- 158  
 DB 177 EGDSDSTYSLSSTLTLSKADYKHKYVACEVTHQGLSPVTKSFNRGEMKQSTIALAL 236  
 QY 159 -----SOVLVESGGGVVQPGRSLRLSCAASGFPFRSFAMHWYRQALGKLEWYA 208  
 DB 227 LPDLFTPTVTKAQVQLVESGGGLVQPGSLRLSCAASGFPFSYAMSWYRQADGKLEWYS 296  
 QY 209 VTSYGSTKYVADSVKGRFTISRDPSSKNTVYLNKMSLPTEDPAVYVCAARDGSLLDYDHX 268  
 DB 297 AISGSGSTYYADSVKGRFTISRDNKNTLTLYLNMSLRADTAIVYCAR-----WGDDGF 351  
 QY 269 YGLDVGKGTITVYVSSGS 286  
 DB 352 YAMDYWGQGTITVYVSSAS 369

Search completed: February 18, 2005, 08:56:01  
 Job time : 84 secs

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## OM protein - protein search, using sw model

Run on: February 18, 2005, 08:47:49 ; Search time 25 Seconds  
(without alignments)  
907.733 Million cell updates/sec

Title: US-09-194-164-14

Perfect score: 1582  
Sequence: 1 EFMKKTATAIAVALAGPATV.....GSEOKLISEEDLNHHHKL 304

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

- Issued Patents AA:\*
- 1: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*
  - 2: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*
  - 3: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*
  - 4: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*
  - 5: /cgn2\_6/prodata/1/1aa/PCTUS\_COMB.pep:\*
  - 6: /cgn2\_6/prodata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1582	100.0	304	3	US-08-862-124-14 Sequence 14, Appl
2	1460.5	92.3	287	3	US-08-862-124-17 Sequence 17, Appl
3	928	58.7	352	4	US-09-203-958A-2 Sequence 2, Appl
4	926.5	58.6	456	4	US-09-495-880A-11 Sequence 11, Appl
5	892	56.4	283	3	US-09-420-592A-6 Sequence 6, Appl
6	892	56.4	283	4	US-09-985-442-6 Sequence 6, Appl
7	892	56.4	283	3	US-09-983-580-6 Sequence 6, Appl
8	887	56.1	263	3	US-09-069-821-3 Sequence 3, Appl
9	887	56.1	263	4	US-09-956-086-3 Sequence 3, Appl
10	887	56.1	263	4	US-09-956-087-3 Sequence 3, Appl
11	865	54.7	354	4	US-09-393-627B-28 Sequence 28, Appl
12	827.5	52.3	240	1	US-08-488-113B-147 Sequence 147, App
13	827.5	52.3	240	1	US-08-477-484B-147 Sequence 147, App
14	827.5	52.3	240	2	US-08-646-360-147 Sequence 147, App
15	827.5	52.3	240	3	US-08-839-765-147 Sequence 147, App
16	827.5	52.3	240	3	US-09-136-389-147 Sequence 147, App
17	827.5	52.3	240	4	US-09-610-838-147 Sequence 147, App
18	827.5	52.3	240	4	US-09-711-485-147 Sequence 147, App
19	808.5	51.1	409	4	US-09-554-765-14 Sequence 14, Appl
20	805	50.9	408	4	US-09-554-765-15 Sequence 15, Appl
21	784	49.6	271	2	US-08-400-115-4 Sequence 4, Appl
22	784	49.6	374	4	US-09-646-028-15 Sequence 15, Appl
23	779.5	49.3	491	4	US-10-011-125A-2 Sequence 2, Appl
24	777	49.1	599	1	US-08-442-542-18 Sequence 18, Appl
25	777	49.1	599	3	US-08-765-469-18 Sequence 18, Appl
26	766	48.4	298	3	US-09-318-661-2 Sequence 2, Appl
27	766	48.4	298	4	US-09-883-758-2 Sequence 2, Appl

28	756	47.8	244	2	US-08-392-338A-13 Sequence 13, Appl
29	756	47.8	244	3	US-09-166-750-13 Sequence 13, Appl
30	756	47.8	244	3	US-09-166-093-13 Sequence 13, Appl
31	756	47.8	244	3	US-09-172-019-13 Sequence 13, Appl
32	756	47.8	244	3	US-09-166-094-13 Sequence 13, Appl
33	756	47.8	244	4	US-09-443-213-13 Sequence 13, Appl
34	755	47.7	239	2	US-08-860-174A-2 Sequence 2, Appl
35	744	47.0	242	2	US-08-392-338A-23 Sequence 23, Appl
36	744	47.0	242	2	US-08-392-338A-23 Sequence 23, Appl
37	744	47.0	242	2	US-08-926-789-14 Sequence 14, Appl
38	744	47.0	242	3	US-09-166-750-23 Sequence 23, Appl
39	744	47.0	242	3	US-09-166-093-23 Sequence 23, Appl
40	744	47.0	242	3	US-09-172-019-23 Sequence 23, Appl
41	744	47.0	242	3	US-09-166-094-23 Sequence 23, Appl
42	744	47.0	242	4	US-09-443-213-23 Sequence 23, Appl
43	744	47.0	244	5	PCT-US93-11138-14 Sequence 14, Appl
44	744	47.0	285	3	US-09-318-661-4 Sequence 4, Appl
45	744	47.0	285	4	US-09-883-758-4 Sequence 4, Appl

## ALIGNMENTS

RESULT 1  
US-08-862-124-14  
Sequence 14, Application US/08862124  
Patent No. 6207153  
GENERAL INFORMATION:  
APPLICANT: Dan, Michael D.  
APPLICANT: Malt, Pradip K.  
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND TITILE OF INVENTION: DETECTION OF CANCERS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster LLP  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/862,124  
FILING DATE: 22-MAY-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Lehnardt, Susan K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 31608-20001.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 304 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-862-124-14  
Query Match 100.0%; Score 1582; DB 3; Length 304;  
Best Local Similarity 100.0%; Pred.No. 2.7e-113;  
Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EFMKKTATAIAVALAGPATVADIVLTOSPTLSLSPERATLSCRASQSVSSSTLAWY 60

Db 1 EFMKTAIAIAVALAGFATVAQADIVLTQSPTLSLSPGERATLSCRASQSVSSSYLAWY 60  
Qy 61 QOKFGQAPRLIIYGASTRATGMPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQOYGSPPQ 120  
Db 61 QOKFGQAPRLIIYGASTRATGMPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQOYGSPPQ 120  
Qy 121 TPQITFGGKTVEIKRTVAAPSVSGSGSGSGSGSQVQLVSGGCVVQPGKSLRLS 180  
Db 121 TPQITFGGKTVEIKRTVAAPSVSGSGSGSGSQVQLVSGGCVVQPGKSLRLS 180  
Qy 181 CAASGPFPRFAMHWKRALGKLEWVAIVSYDSTKYADSVKGRFTISRDTSKNTVYL 240  
Db 181 CAASGPFPRFAMHWKRALGKLEWVAIVSYDSTKYADSVKGRFTISRDTSKNTVYL 240  
Qy 241 KNSLRTEPTDAVYYCARDOSLLGDYDHYGLDVGKGTIVVSSGSEOKLISEEDLNHHH 300  
Db 241 KNSLRTEPTDAVYYCARDOSLLGDYDHYGLDVGKGTIVVSSGSEOKLISEEDLNHHH 300  
Qy 301 HHKL 304  
Db 301 HHKL 304

## RESULT 2

US-08-862-124-17  
; Sequence 17, Application US/08862124  
; Patent No. 6207153  
; GENERAL INFORMATION:  
; APPLICANT: Dan, Michael D.  
; APPLICANT: Maiti, Pradip K.  
; APPLICANT: Kaplan, Howard A.  
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT  
; TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE  
; TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND  
; NUMBER OF INVENTION: DETECTION OF CANCERS  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster LLP  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/862,124  
; FILING DATE: 22-MAY-1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lemhard, Susan K.  
; REGISTRATION NUMBER: 33,943  
; REFERENCE/DOCKET NUMBER: 31608-20001.20  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 813-5600  
; TELEFAX: (650) 494-0792  
; TELETYPE: 706141  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 287 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-862-124-17

Query Match 92.3%; Score 1460.5; DB 3; Length 287;  
Best Local Similarity 93.8%; Pred. No. 4.7e-104;  
Matches 285; Conservative 0; Mismatches 2; Indels 17; Gaps 1;

Qy 1 EFMKTAIAIAVALAGFATVAQADIVLTQSPTLSLSPGERATLSCRASQSVSSSYLAWY 60  
Db 1 EFMKTAIAIAVALAGFATVAQADIVLTQSPTLSLSPGERATLSCRASQSVSSSYLAWY 60  
Qy 61 QOKFGQAPRLIIYGASTRATGMPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQOYGSPPQ 120  
Db 61 QOKFGQAPRLIIYGASTRATGMPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQOYGSPPQ 120  
Qy 121 TPQITFGGKTVEIKRTVAAPSVSGSGSGSGSQVQLVSGGCVVQPGKSLRLS 180  
Db 121 TPQITFGGKTVEIKRTVAAPSVSGSGSGSGSQVQLVSGGCVVQPGKSLRLS 180  
Qy 181 CAASGPFPRFAMHWKRALGKLEWVAIVSYDSTKYADSVKGRFTISRDTSKNTVYL 240  
Db 181 CAASGPFPRFAMHWKRALGKLEWVAIVSYDSTKYADSVKGRFTISRDTSKNTVYL 240  
Qy 241 KNSLRTEPTDAVYYCARDOSLLGDYDHYGLDVGKGTIVVSSGSEOKLISEEDLNHHH 300  
Db 241 KNSLRTEPTDAVYYCARDOSLLGDYDHYGLDVGKGTIVVSSGSEOKLISEEDLNHHH 300  
Qy 301 HHKL 304  
Db 284 HHKL 287

## RESULT 3

US-09-203-958A-2  
; Sequence 2, Application US/09203958A  
; Patent No. 6682928  
; GENERAL INFORMATION:  
; APPLICANT: KELLER, Tibor  
; APPLICANT: GOLDSTEIN, Joel  
; APPLICANT: GRAZIANO, Robert  
; APPLICANT: DEO, Yashwant M.  
; TITLE OF INVENTION: CELLS EXPRESSING ANTI-FC RECEPTOR  
; TITLE OF INVENTION: BINDING COMPONENTS  
; FILE REFERENCE: MXI-099CPA  
; CURRENT APPLICATION NUMBER: US/09/203,958A  
; PRIOR FILING DATE: 1998-12-02  
; PRIOR APPLICATION NUMBER: 60/067232  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
US-09-203-958A-2

Query Match 58.7%; Score 928; DB 4; Length 352;  
Best Local Similarity 66.4%; Pred. No. 2.8e-63;

Matches 192; Conservative 26; Mismatches 45; Indels 26; Gaps 5;

Qy 18 ATVAQADIVLTQSPTLSLSPGERATLSCRASQSVSSSYLAWYQOKFGQAPRLII 72  
Db 32 AOPASDIQULTQSSLSASVGDVITCKSSQSVLYSSNQKTLAWYQOKFGQAPRLII 91  
Qy 73 YGASTRATGMPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQOYGSPPQTPQITFGGKT 132  
Db 92 YMASTRSGVPSRSGSGSGTDFTLTISRLEPEDFAVYYCHQYLSS-----WTFGQSTKV 146  
Qy 133 EIKRTVAAPSVSGSGSGSGSGSQVQLVSGGCVVQPGKSLRLSCAASGPFPRSF 192  
Db 147 EIKS-----SGGGSGSGSGSGSGSQVQLVSGGCVVQPGKSLRLSCSSGFTFSDNY 199  
Qy 193 MEWVRQALGKLEWVAIVSYDSTKYADSVKGRFTISRDTSKNTVYLKNSLRTEPTDAV 252  
Db 200 MEWVRQALGKLEWVAIVSYDSTKYADSVKGRFTISRDTSKNTVYLFLQNDLSRPEDTGV 259  
Qy 253 YYCARDOSLLGDYDHYGLDVGKGTIVVSSG-----SEOKLISEEDLN 297

Db 260 YFCAR-----GYRYEGANDYWGQGTPTVSSPRLQVDBQKLSBEDLN 303

## RESULT 4

US-09-495-880A-11  
Sequence 11, Application US/09495880A

GENERAL INFORMATION:  
PATENT NO. 6667150  
APPLICANT: RUDERT, FRITZ  
APPLICANT: GE, LIMING  
APPLICANT: ILAG, VIC  
TITLE OF INVENTION: NOVEL METHOD AND PHASE FOR THE IDENTIFICATION OF  
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING MEMBERS OF A MULTIMERIC  
TITLE OF INVENTION: (POLY) PEPTIDE COMPLEX  
FILE REFERENCE: MORPHO/9  
CURRENT APPLICATION NUMBER: US/09/495,880A  
CURRENT FILING DATE: 2000-02-01  
PRIOR APPLICATION NUMBER: PCT/EP98/04836  
PRIOR FILING DATE: 1998-08-03  
PRIOR APPLICATION NUMBER: EP 97 11 3319.4  
PRIOR FILING DATE: 1997-08-01  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 11  
LENGTH: 456  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: ompA-FLAG-scFv (anti-  
OTHER INFORMATION: HAg)-gene IIIs encoded by phage vector fHag1a (circular)  
US-09-495-880A-11

Query Match 58.6%; Score 926.5; DB 4; Length 456;  
Best Local Similarity 63.1%; Pred. No. 4,9e-63;

Matches 190; Conservative 37; Mismatches 49; Indels 25; Gaps 6;

QY 3 MKKTAIAIATVAGAFATVQA---DIVLTQSPGTLISLSPGERATLSCRAQSQVSS---- 55  
DB 1 MKKTAIAIATVAGAFATVQAQADYKDIWMTQSPSSLTVTAAGEVYVMTSCISSQSLFNSGKQK 60  
QY 56 -YLAWYQKPGQAPRLIYGASTRATGMPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQO 114  
DB 61 NLTLYQKPGQAPRLIYMASTRSGVDRFTGSGSGTDFTLTISRVAEDLAVYYCQN 120  
QY 115 YGSSPQRTQITFGGSGTQVEIKRTVAAP-----VSGGSGSGSGSGSGSGSQVQLVES 166  
DB 121 DYSNP-----LTFGGGSKLELKRAGGGSGSGSGSGSGSGSGSGSGSGSGSGSGSVQLVES 176  
QY 167 GGGVQVQPRSLRLSCAASGFFPRSRFAMHVRQALGKLEWAVISYDGS TKTYAASVKQR 226  
DB 177 GGDVLPKPGSLRLSCAASGFSFSYGMWVRQTPDKLEWAVTISNGGYTYTPDSVKQR 236  
QY 227 FTISDTSKNTYYLKNLSRTEDTAVYYCARDQSLGDHYGGLDVGKGTITVYSSGS 286  
DB 227 FTISDNKNTIYLYOMSSLSKSDSAMYCARER-----YDE-NGRAYMGQGLITVYSAG 291  
QY 287 E 287  
DB 292 E 292

## RESULT 5

US-09-420-592A-6  
Sequence 6, Application US/09420592A

GENERAL INFORMATION:  
PATENT NO. 6333396  
APPLICANT: Filpula, David R.  
APPLICANT: Wang, Maoliang  
APPLICANT: Whitlow, Marc D.  
TITLE OF INVENTION: No. 6333396e1 Method for Targeted Delivery of Nucleic Acids  
FILE REFERENCE: 0977.2300001  
CURRENT APPLICATION NUMBER: US/09/420,592A  
CURRENT FILING DATE: 1999-10-19

PRIOR APPLICATION NUMBER: 60/104,949

PRIOR FILING DATE: 1998-10-20

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 6

LENGTH: 283

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Kabat

NAME/KEY: UNSURE

LOCATION: (232)

OTHER INFORMATION: May be any amino acid.

NAME/KEY: UNSURE

LOCATION: (239)

OTHER INFORMATION: May be any amino acid.

US-09-420-592A-6

Query Match 56.4%; Score 892; DB 3; Length 283;  
Best Local Similarity 66.3%; Pred. No. 1.2e-60;

Matches 181; Conservative 29; Mismatches 47; Indels 16; Gaps 5;

QY 24 DIVLTQSPGTLISLSPGERATLSCRAQSQV--SSYLAWYQKPGQAPRLIYGASTRATG 81  
DB 1 DIWMTQSPSSLTASASVDYVITTCRASQSLVSIISNLTAWYQKPGQAPRLIYAASSLSESG 60  
QY 82 MDRFRSGSGSGTDFTLTISRLEPEDFAVYYCQVGSPPQRTQITFGGSGTQVEIKRTVAAP 141  
DB 61 VPSRFSGSGSGTDFTLTISRLEPEDFAVYYCQVNS--LPEWTTGQGTQVEIKGS----- 113  
QY 142 SVSGGSGSGSGSGSGSQVQLVESGGGVQPRSLRLSCAASGFFPRSRFAMHVRQALG 201  
DB 114 -TSGSGKPRGSEGGSTKREYGVESGGGLVQSGSLRLSCAASGTFSSYAMSWVRQARG 171  
QY 202 KLEWAVAVIS--YDGSITKYADSVKGRFTISDTSKNTYYLKNLSRTEDTAVYYCARDQ 259  
DB 172 KLEWAVSYSGKTDGSGTYADSVKGRFTISRDNKNTIYLYOMSLRAEDTAVYYCARGR 231  
QY 260 ---SLGSDYDHYGGLDVGKGTITVYSSGSEK 289  
DB 232 XGXSLSGXYHYHYPDWGQGTITVSSKKKK 264

## RESULT 6

US-09-985-442-6  
Sequence 6, Application US/09985442

PATENT NO. 6692942

GENERAL INFORMATION:

APPLICANT: Filpula, David R.

APPLICANT: Wang, Maoliang

APPLICANT: Whitlow, Marc D.

TITLE OF INVENTION: No. 6692942e1 Method for Targeted Delivery of Nucleic Acids

FILE REFERENCE: 0977.2300003

CURRENT APPLICATION NUMBER: US/09/985,442

CURRENT FILING DATE: 2001-11-02

PRIOR APPLICATION NUMBER: 09/420,592

PRIOR FILING DATE: 1998-10-19

PRIOR APPLICATION NUMBER: 60/104,949

PRIOR FILING DATE: 1998-10-20

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 6

LENGTH: 283

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Kabat

NAME/KEY: UNSURE





APPLICATION NUMBER: US 60/050,472  
FILING DATE: 23-JUN-1997  
APPLICATION NUMBER: US 60/044,449  
FILING DATE: 30-APR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: KIM, JUDITH U.  
REGISTRATION NUMBER: 40,679  
REFERENCE/DOCKET NUMBER: 0977.2280003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)371-2600  
TELEFAX: (202)371-2540  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 263 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-956-087-3

Query Match 56.1%; Score 887; DB 4; Length 263;  
Best Local Similarity 67.2%; Pred. No. 2,7e-60;  
Matches 180; Conservative 27; Mismatches 45; Indels 16; Gaps 5;

QY 24 DIVLTQSPGTLSPGSRATLSCRASQSV--SSSTIAMTQOKPGQAPRLITYGASTRATG 81  
DB 1 DIQMTQSPSLTAVAGKVTMSCKSSQSLNSGNQKNTLYTQOKPGQAPRLITYGAST 60  
QY 82 MPDRFSGSGSGTDFTLTISRLEPEDPAVYYCOQYSSPOTPOITFGGSKVEIKRTVAAP 141  
DB 61 VSRKSGSGSGTDFTLTISRLEPEDPAVYYCOQYSSPOTPOITFGGSKVEIKRTVAAP 113  
QY 142 SVSGGGSGGGSGGGGGVQVLESQGVQVOPGRSIRLSCAASGPFPSFAMHWYRQALG 201  
DB 114 --TSGSGKRGSGEGSTKGEVQLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQARG 171  
QY 202 KLEWNAVVS--YDSSTKYADSVYGRFTISRDTSKNTLYLKNNSLRTEDTAVYYCARQ 259  
DB 172 KLEWNAVSVISGKTDGISTYVADSVKGRFTISRDNKNLYLQMSLRADTAVYYCARGR 231  
QY 260 --SLGADYDHYGLDVGWKGTTVYS 284  
DB 232 XGSLSGKYYHYHFDYWGCGTLVTVSS 259

RESULT 11  
US-09-393-627B-28  
Sequence 28, Application US/09393627B  
Patent No. 6455314

GENERAL INFORMATION:  
APPLICANT: Wickham, Thomas J.  
APPLICANT: Kovesdi, Imre  
APPLICANT: Roelivink, Petrus W.  
APPLICANT: Bruder, Joseph T.  
TITLE OF INVENTION: Alternatively Targeted Adenovirus  
FILE REFERENCE: 202345  
CURRENT APPLICATION NUMBER: US/09/393,627B  
CURRENT FILING DATE: 1999-09-10  
PRIOR APPLICATION NUMBER: US 60/099,851  
PRIOR FILING DATE: 1998-09-11  
PRIOR APPLICATION NUMBER: US 60/136,529  
PRIOR FILING DATE: 1999-05-28  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn Ver. 2.2  
SEQ ID NO 28  
LENGTH: 354  
TYPE: PRT  
ORGANISM: Anti-HA ScFv fused in frame with 2 C-terminal myc epitopes and  
PDGF receptor transmembrane anchor (Anti-HA pseudo-receptor)  
US-09-393-627B-28

Query Match 54.7%; Score 865; DB 4; Length 354;

Best Local Similarity 61.2%; Pred. No. 1.8e-58;  
Matches 172; Conservative 42; Mismatches 45; Indels 22; Gaps 6;

QY 23 ADIVLTQSPGTLSPGSRATLSCRASQSVSSS-----YLAWQOKPGQAPRLITYGAST 77  
DB 26 ADIVLTQSPSLTAVAGKVTMSCKSSQSLNSGNQKNTLYTQOKPGQAPRLITYGAST 85  
QY 78 RATGMPDRFSGSGSGTDFTLTISRLEPEDPAVYYCOQYSSPOTPOITFGGSKVEIKRT 137  
DB 86 RSGVDPDRFTGSGSGRDTLTISRVAEDLAIVYYCQNNNSHP---LTFGAGTKLELR- 140  
QY 138 VAAPSVSGGGSGGGSGGGGGVQVLESQGVQVOPGRSIRLSCAASGPFPSFAMHWYR 197  
DB 141 -----AGGGSGGGSGGGGGVQVLESQGVQVOPGRSIRLSCAASGFTFSYAMSWVR 194  
QY 188 QALGKLEWNAVVISYDSTKYADSVYGRFTISRDTSKNTLYLKNNSLRTEDTAVYYCAR 257  
DB 195 QTPNRLIEWVPTLIRGGSVYTPYDGVKGRFTISKNNAKNTLYLQMSLRSEDTAVYYCAK 254  
QY 258 DQSLGADYDHYGLDVGWKGTTVYS--SGSEKLISEEDLN 297  
DB 255 RET---FDE-KGFAYWGCGTLVTVSSAAAEKLISEEDLN 290

RESULT 12  
US-08-488-113B-147  
Sequence 147, Application US/08488113B  
Patent No. 5744580

GENERAL INFORMATION:  
APPLICANT: Belter, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studinka, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,113B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155

TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 147:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 amino acids  
TYPE: amino acid  
TOPOLOGY: 1linear  
MOLECULE TYPE: protein  
US-08-488-113B-147

Query Match 52.3%; Score 827.5; DB 1; Length 240;  
Best Local Similarity 61.7%; Pred. No. 8.5e-56;  
Matches 161; Conservative 37; Mismatches 42; Indels 21; Gaps 5;

QY 24 DIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIYGASTRATGMP 83  
DB 1 DIQMTQSPSSLSASVDGRVTITCRASQDI-NSYLSWFOQPKAPKTLIRANRLSGVP 59  
QY 84 DRFGSGSGTDTLTISRLEPEDFAVYVCOQYSSPQTQITFGGKTKEIKRTVAAPSV 143  
DB 60 SRFSSGSGTDTLTISRLEPEDFAVYVCOQYDESPW-----TFGGTKLEMK----- 107  
QY 144 SGGGSGGGGSGGGGSGGVQVLVESGGGVVQPGRLSLRSCAAGFPFRSFAMHWVROALGKG 203  
DB 108 -GGGSGGGGSGGGGSGGVQVLVESGGGVVQPGRLSLRSCAAGFPFRSFAMHWVROALGKG 166  
QY 204 LEWVAIVSDSTKYKADSVKGRFTISRDTSKNTYVLRKNSLRTEPTAVYICARDQSLIG 263  
DB 167 LEWKMVINTHTGEPTAVDFKGRFTFSLDSSKNTAVLQINSIRAEPTAVYFCR-----R 221  
QY 264 DYDHYGLDVGKGTIVTVSS 284  
DB 222 GYDWF--DVWGQGTIVTVSS 240

RESULT 13  
US-08-477-484B-147  
Sequence 147, Application US/08477484B  
Patent No. 5756699  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,484B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/968,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 147:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 amino acids  
TYPE: amino acid  
TOPOLOGY: 1linear  
MOLECULE TYPE: protein  
US-08-477-484B-147

Query Match 52.3%; Score 827.5; DB 1; Length 240;  
Best Local Similarity 61.7%; Pred. No. 8.5e-56;  
Matches 161; Conservative 37; Mismatches 42; Indels 21; Gaps 5;

QY 24 DIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIYGASTRATGMP 83  
DB 1 DIQMTQSPSSLSASVDGRVTITCRASQDI-NSYLSWFOQPKAPKTLIRANRLSGVP 59  
QY 84 DRFGSGSGTDTLTISRLEPEDFAVYVCOQYSSPQTQITFGGKTKEIKRTVAAPSV 143  
DB 60 SRFSSGSGTDTLTISRLEPEDFAVYVCOQYDESPW-----TFGGTKLEMK----- 107  
QY 144 SGGGSGGGGSGGGGSGGVQVLVESGGGVVQPGRLSLRSCAAGFPFRSFAMHWVROALGKG 203  
DB 108 -GGGSGGGGSGGGGSGGVQVLVESGGGVVQPGRLSLRSCAAGFPFRSFAMHWVROALGKG 166  
QY 204 LEWVAIVSDSTKYKADSVKGRFTISRDTSKNTYVLRKNSLRTEPTAVYICARDQSLIG 263  
DB 167 LEWKMVINTHTGEPTAVDFKGRFTFSLDSSKNTAVLQINSIRAEPTAVYFCR-----R 221  
QY 264 DYDHYGLDVGKGTIVTVSS 284  
DB 222 GYDWF--DVWGQGTIVTVSS 240

RESULT 14  
US-08-646-360-147  
Sequence 147, Application US/08646360  
Patent No. 5837491  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,360  
FILING DATE: 13-MAY-1996  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/05348

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/ FILING DATE: 12-MAY-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/064,691
/ FILING DATE: 12-MAY-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/988,430
/ FILING DATE: 09-DEC-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 19-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 200-70.P4
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/707-8889
/ TELEFAX: 312/707-9155
/ TELEX: 650 388-1248
/ INFORMATION FOR SEQ ID NO. 147:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 240 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/
/ US-08-646-360-147

```

Query Match	52.3%	Score 827.5	DB 2	Length 240
Best Local Similarity	61.7%	Pred. No. 8.5e-56		
Matches 161	Conservative 37	Mismatches 42	Indels 21	Gaps 5

```

QY      241LTLSPPTLLSPERARLLSCRASOSVSSSYSLAMWQKGPAPRLITICASTPATGMP  83
Db      1DIQMOSPSSLASVQDRVITTCRASQDI-NSLYSLFPQKQKAPKILITRANLSEGV  59

QY      84DRPSGSGSTDTLLTISRLEPDPFAVYYCOQYGSSPQTPQITFGGKTKVEIKRTVAAPSV  143
Db      60SRPSGSGSGTDTLLTIRISLQYEDFQIYYCOQYDESPW----TFGGGTLEMK-----  107

QY      144SGGGSGGGSGGGSGGGSGOVLVSGGGGVOPRPSLRSLSCAASGPFPRSPFAMHWPRQALGK  203
Db      108-GGGSGGGSGGGSGGGSGSEIOLVDSGGGLVAPGSGVAISCAASGYTFYINGMWRQAQKGG  166

QY      204LEWVAVISYDGSSTKYADSVKGRFTTISRDTSKNTVYLKMSLIRPEDIYAVYYCARDOSILG  263
Db      167LEWGMGINTHTGEPFLYADSFKGRFPFLSDDSKNTATYLQINSIRAEADTNAVYFCIR-----R  221

QY      264DYDHYGLDVMKGGKTTVYSS  284
Db      222GYDMYF--DVWGQGTITVYSS  240

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RESULT 15  
US-08-839-765-147

Patent No. 6146631  
 GENERAL INFORMATION:  
 APPLICANT: Better, Marc D.  
 APPLICANT: Carroll, Stephen F.  
 APPLICANT: Studnika, Gary M.  
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
 TITLE OF INVENTION: Proteins  
 NUMBER OF SEQUENCES: 169  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
 STREET: 500 West Madison Street, 34th floor  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60661  
 COMPUTER READABLE FORM:

```

1 MEDIUM TYPE: Floppy disk
2 COMPUTER: IBM PC compatible
3 OPERATING SYSTEM: PC-DOS/MS-DOS
4 SOFTWARE: PatentIn Release #1.0, Version #1.25
5 CURRENT APPLICATION DATA:
6 APPLICATION NUMBER: US/08/839,765
7 FILING DATE: 15-APR-1997
8 CLASSIFICATION: 530
9 PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: US 08/425,336
11 FILING DATE: 18-APR-1995
12 PRIOR APPLICATION DATA:
13 APPLICATION NUMBER: US 08/064,691
14 FILING DATE: 12-MAY-1993
15 PRIOR APPLICATION DATA:
16 APPLICATION NUMBER: US 07/988,430
17 FILING DATE: 09-DEC-1992
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: US 07/901,707
20 FILING DATE: 19-JUN-1992
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: US 07/787,567
23 FILING DATE: 04-NOV-1991
24 ATTORNEY/AGENT INFORMATION:
25 NAME: McNicholas, Janet M.
26 REGISTRATION NUMBER: 32,918
27 REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: 312/707-8889
30 TELEFAX: 312/707-9155
31 TELEX: 650 388-1248
32 INFORMATION FOR SEQ ID NO: 147:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 240 amino acids
35 TYPE: amino acid
36 TOPOLOGY: linear
37 MOLECULE TYPE: protein
38 JS-08-839-765-147

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Query Match	52.3%	Score 827.5;	DB 3;	length 240;
Best Local Similarity	61.7%;	Pred. No. 8.5e-56;		
Matches 161; Conservative	37;	Mismatches 42;	Indels 21;	Gaps 5;

QY 24VLNDSPPTLSLSPGEPATLSCPRASVSSSYLAWQOKGQAPRLITVASTPATGMP 83  
 1 D1QMTQSPBSLSASVGRKTYITICRASQDI -NSIYLSWFQOKGKAPKILITRANLBSGVP 59  
 QY 84DRPSGSGSTDPDLLTITLSRLPEDFAVVYCCQYGSSPQTPQITFGGKTKVEIKRTVAAPSV 143  
 60SRFSGSGSGSTDPDLLTITLSLOYEDFGIYYCCQYDSSPW----TFAGGKTKLEMK----- 107  
 Db 144SGGSGSGSGSGSGSGSOVLVESGGGVYQPERSLRLSCAASGFFRFSFAMHWNRQALGK 203  
 108-GGGSGSGSGSGSGSGSEIQLVQSGGGLVKKPGGSVKISCAASGYFTYIGMHWQAQAGK 166  
 Db 204LEMWAVISYDGSSTKYADSVKGRFPIISKDTSKNIVYLKMSLRTEDPAVYVYCCARDOSILG 263  
 167LEMWGMINTHTGEPTVYADSPKGRFTFSLDSKMTAIVQLINSLRADPTAVVYFCFR-----R 221  
 Db 264DYDHTYGLDVMWKGKTTTVYSS 284  
 222GYDWYF--DVMGQGITTVYSS 240

Search completed: February 18, 2005, 08:58:29  
Job time : 26 secs



GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: February 18, 2005, 08:54:45 ; Search time 73 Seconds  
(without alignments)  
1362.757 Million cell updates/sec

Title: US-09-194-164-14

Perfect score: 1582

Sequence: 1 EFMKKTALATVALAGRTV.....GSEOKLISEEDLNHHHKL 304

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1380268 seqs, 327241040 residues

Total number of hits satisfying chosen parameters: 1380268

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/FCI\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*  
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8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
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13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
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18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1582	100.0	304	10	US-09-782-397-14 Sequence 14, Appl
2	1582	100.0	304	15	US-10-651-453-14 Sequence 14, Appl
3	1460.5	92.3	287	15	US-09-782-397-17 Sequence 17, Appl
4	1460.5	92.3	287	15	US-10-651-453-17 Sequence 17, Appl
5	928	58.7	352	10	US-09-203-958A-2 Sequence 21, Appl
6	928.5	58.6	456	15	US-10-634-862-11 Sequence 11, Appl
7	892	56.4	283	9	US-09-983-580-6 Sequence 6, Appl
8	892	56.4	283	9	US-09-985-442-6 Sequence 6, Appl
9	887	56.1	263	9	US-09-956-086-3 Sequence 3, Appl
10	866.5	54.8	263	9	US-09-956-087-3 Sequence 3, Appl
11	866.5	54.8	630	15	US-10-422-628-48 Sequence 48, Appl
12	866.5	54.8	639	15	US-10-422-628-16 Sequence 16, Appl
13	863.5	54.6	277	15	US-10-422-628-43 Sequence 43, Appl

14	857.5	54.2	279	15	US-10-409-938-21	Sequence 21, Appl
15	849.5	53.7	252	15	US-10-423-847-10	Sequence 10, Appl
16	849.5	53.7	253	15	US-10-423-847-14	Sequence 14, Appl
17	849.5	53.7	253	15	US-10-423-847-11	Sequence 11, Appl
18	849.5	53.7	254	15	US-10-423-847-17	Sequence 17, Appl
19	847	53.5	239	15	US-10-423-847-18	Sequence 18, Appl
20	827.5	52.3	240	14	US-10-127-890-147	Sequence 147, App
21	824.5	52.1	247	15	US-10-423-847-13	Sequence 13, Appl
22	824	52.1	443	13	US-10-006-773-2	Sequence 2, Appl
23	824	52.1	443	13	US-10-006-771A-2	Sequence 2, Appl
24	810	51.2	4852	15	US-10-412-406-3	Sequence 33, Appl
25	808.5	51.0	409	15	US-10-353-721-14	Sequence 14, Appl
26	807.5	51.0	502	15	US-10-679-620-88	Sequence 88, Appl
27	806.5	51.0	663	15	US-10-412-406-32	Sequence 32, Appl
28	805	50.9	408	15	US-10-353-721-15	Sequence 15, Appl
29	803.5	50.8	252	9	US-09-971-543-1	Sequence 1, Appl
30	784.5	49.6	364	16	US-10-829-388-11	Sequence 11, Appl
31	784.5	49.6	370	16	US-10-829-388-1	Sequence 1, Appl
32	784	49.6	271	10	US-09-226-157-4	Sequence 4, Appl
33	784	49.6	374	14	US-10-335-394-15	Sequence 15, Appl
34	779.5	49.3	491	13	US-10-011-125-2	Sequence 2, Appl
35	770	48.7	256	15	US-10-418-182-2	Sequence 2, Appl
36	769	48.6	492	14	US-10-207-655-344	Sequence 344, App
37	767.5	48.5	543	14	US-10-207-655-346	Sequence 346, App
38	767	48.5	298	9	US-10-207-655-345	Sequence 345, App
39	766	48.4	298	9	US-09-883-758-2	Sequence 2, Appl
40	766	48.4	556	14	US-10-207-655-268	Sequence 268, App
41	762.5	48.2	431	14	US-10-013-173-4	Sequence 4, Appl
42	762.5	48.2	431	14	US-10-150-762-4	Sequence 4, Appl
43	762.5	48.2	431	14	US-10-244-821-4	Sequence 43, App
44	761	48.1	258	14	US-10-207-655-343	Sequence 254, App
45	759.5	48.0	271	14	US-10-207-655-254	

## ALIGNMENTS

RESULT 1  
US-09-782-397-14  
; Sequence 14, Application US/09782397  
; Publication No. US2003002179A1  
; GENERAL INFORMATION:  
APPLICANT: Dan, Michael D.  
Kaplan, Howard A.  
Malt, Pradip K.  
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT  
SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE  
FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND  
DETECTION OF CANCERS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster LLP  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/782,397  
FILING DATE: 13-Feb-2001  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/862,124  
FILING DATE: 1997-05-22  
ATTORNEY/AGENT INFORMATION:  
NAME: Lehnardt, Susan K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 31608-20001.20

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 304 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-782-397-14

Query Match      100.0%; Score 1582; DB 10; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.8e-95;
Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EFMKKTAAIAVAVLAGFATVAADIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAMY 60
DB 1 EFMKKTAAIAVAVLAGFATVAADIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAMY 60
QY 61 OQPGQAPRLIIYGASTATGMPDRFSSGSGGTDFTLTISRLEPEDFAVYYCQOYGSSPQ 120
DB 61 OQPGQAPRLIIYGASTATGMPDRFSSGSGGTDFTLTISRLEPEDFAVYYCQOYGSSPQ 120
QY 121 TPQITFGGGTKVEIKRTVAAPSVSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGG 180
DB 121 TPQITFGGGTKVEIKRTVAAPSVSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGG 180
QY 181 CAASGPPRSPFAMHVRQALGKLEWVAIVSYDSTKYVAASVKGRFTISRPTSKNTVYL 240
DB 181 CAASGPPRSPFAMHVRQALGKLEWVAIVSYDSTKYVAASVKGRFTISRPTSKNTVYL 240
QY 241 KNSLRTEDTAVYYCARQDSLLGDYDHYGDLVWGKGTITVYSSGSEQKLISEEDLNHHH 300
DB 241 KNSLRTEDTAVYYCARQDSLLGDYDHYGDLVWGKGTITVYSSGSEQKLISEEDLNHHH 300
QY 301 HHKL 304
DB 301 HHKL 304

RESULT 2
US-10-651-453-14
; Sequence 14, Application US/10651453
; Publication No. US20040091484A1
; GENERAL INFORMATION:
; APPLICANT: Maici, Michael D.
; APPLICANT: Dan, Michael P.
; APPLICANT: Kaplan, Howard A.
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT SPECIFICALLY DETECT CANCER CELLS,
; TITLE OF INVENTION: NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PRO
; FILE REFERENCE: 316082000103
; CURRENT APPLICATION NUMBER: US/10/651,453
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US 09/782,397
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: US 08/862,124
; PRIOR FILING DATE: 1997-05-22
; PRIOR APPLICATION NUMBER: US 08/657,449
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-651-453-14

Query Match      100.0%; Score 1582; DB 15; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.8e-95;
Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 EFMKKTAAIAVAVLAGFATVAADIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAMY 60
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QY 61 OQPGQAPRLIIYGASTATGMPDRFSSGSGGTDFTLTISRLEPEDFAVYYCQOYGSSPQ 120
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QY 121 TPQITFGGGTKVEIKRTVAAPSVSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGG 180
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DB 181 CAASGPPRSPFAMHVRQALGKLEWVAIVSYDSTKYVAASVKGRFTISRPTSKNTVYL 240
QY 241 KNSLRTEDTAVYYCARQDSLLGDYDHYGDLVWGKGTITVYSSGSEQKLISEEDLNHHH 300
DB 241 KNSLRTEDTAVYYCARQDSLLGDYDHYGDLVWGKGTITVYSSGSEQKLISEEDLNHHH 300
QY 301 HHKL 304
DB 301 HHKL 304

RESULT 3
US-09-782-397-17
; Sequence 17, Application US/09782397
; Publication No. US20030021779A1
; GENERAL INFORMATION:
; APPLICANT: Maici, Michael D.
; APPLICANT: Kaplan, Howard A.
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H1, THAT
; SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
; FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
; DETECTION OF CANCERS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESS: Morrison & Foerster LLP
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/782,397
; FILING DATE: 13-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/862,124
; FILING DATE: 1997-05-22
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 31608-20001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 287 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
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US-09-782-397-17

Query Match 92.3%; Score 1460.5; DB 10; Length 287;

Best Local Similarity 93.8%; Pred. No. 1.4e-87;

Matches 285; Conservative 0; Mismatches 2; Indels 17; Gaps 1;

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Db 164 CAASGPPRSPAMHWRQALGKLEWVAVISYDGSSTKYAASVKGRFTISRDTSKNTVYL 223
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Qy 301 HHKL 304
Db 284 HHKL 287
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RESULT 4

US-10-651-453-17

; Sequence 17, Application US/10651453

; Publication No. US20040091484a1

; GENERAL INFORMATION:

; APPLICANT: Dan, Michael D.

; APPLICANT: Maltl, Pradip K.

; APPLICANT: Kaplan, Howard A.

; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT SPECIFICALLY DETECT CANCER CELLS,

; TITLE OF INVENTION: NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PRO

; FILE REFERENCE: 316082000103

; CURRENT APPLICATION NUMBER: US/10/651,453

; PRIOR FILING DATE: 2003-08-29

; PRIOR APPLICATION NUMBER: US 09/782,397

; PRIOR FILING DATE: 2001-02-13

; PRIOR APPLICATION NUMBER: US 08/862,124

; PRIOR FILING DATE: 1997-05-22

; PRIOR APPLICATION NUMBER: US 08/657,449

; PRIOR FILING DATE: 1996-05-22

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 17

; LENGTH: 287

; TYPE: PRT

; ORGANISM: Homo Sapiens

US-10-651-453-17

Query Match 92.3%; Score 1460.5; DB 15; Length 287;

Best Local Similarity 93.8%; Pred. No. 1.4e-87;

Matches 285; Conservative 0; Mismatches 2; Indels 17; Gaps 1;

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Qy 1 EFMKTAIAIVAGFATVAQADIVLTQSPTLSLSPGERATLSCRASQSVSSSYLAMY 60
Db 1 EFMKTAIAIVAGFATVAQADIVLTQSPTLSLSPGERATLSCRASQSVSSSYLAMY 60
Qy 61 QOKPGQARLLIYGASTATGMPDRFSGSGGCTDFTLTISRLEPDPFAVYYCOQYSSSPQ 120
Db 61 QOKPGQARLLIYGASTATGMPDRFSGSGGCTDFTLTISRLEPDPFAVYYCOQYSSSPQ 120
Qy 121 TPQITFGGCTKVEIKRTVAAPSVSQGGSGGGGSGGSGGQVQVLSGGGQVQPGRSRLRS 180
Db 121 TPQITFGGCTKVEIKRTVAAPSVSQGGSGGGGSGGSGGQVQVLSGGGQVQPGRSRLRS 180
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Db 121 TPQITFGGCTKVEIKRTVAAPSVSQGGSGGGGSGGSGGQVQVLSGGGQVQPGRSRLRS 163

Qy 181 CAASGPPRSPAMHWRQALGKLEWVAVISYDGSSTKYAASVKGRFTISRDTSKNTVYL 240

Db 164 CAASGPPRSPAMHWRQALGKLEWVAVISYDGSSTKYAASVKGRFTISRDTSKNTVYL 223

Qy 241 KMSLRTEDTAVYYCARDQSLGDYDHYGLDWKGGTTVYSSGSEQKLISEEDLNHHH 300

Db 224 KMSLRTEDTAVYYCARDQSLGDYDHYGLDWKGGTTVYSSGSEQKLISEEDLNHHH 283

Qy 301 HHKL 304

Db 284 HHKL 287

RESULT 5

US-09-203-958A-2

; Sequence 2, Application US/09203958A

; Publication No. US20030039641A1

; GENERAL INFORMATION:

; APPLICANT: Keler, Tibor

; APPLICANT: GOLDSTEIN, Joel

; APPLICANT: GRAZIANO, Robert

; APPLICANT: DEO, Vashwant M.

; TITLE OF INVENTION: CELLS EXPRESSING ANTI-FC RECEPTOR

; FILE REFERENCE: MXI-099CPA

; CURRENT APPLICATION NUMBER: US/09/203,958A

; CURRENT FILING DATE: 1998-12-02

; PRIOR APPLICATION NUMBER: 60/067232

; PRIOR FILING DATE: 1997-12-02

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 352

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic construct

US-09-203-958A-2

Query Match 58.7%; Score 928; DB 10; Length 352;

Best Local Similarity 66.4%; Pred. No. 8.3e-53;

Matches 192; Conservative 26; Mismatches 45; Indels 26; Gaps 5;

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Qy 18 ATVAQADIVLTQSPTLSLSPGERATLSCRASQSVSSSYLAMYQOKPGQARLLI 72
Db 32 AQPASDITQLTQSPESLSASVGDRTITCKSSQSVLVSNNKNTLAWYQOKPGKAPKLLI 91
Qy 73 YGASTATGMPDRFSGSGGCTDFTLTISRLEPDPFAVYYCOQYSSPOTPTFGGCTKV 132
Db 92 YWASTRESGVPSRFSGSGGCTDFTLTISRLEPDPFAVYYCOQYSSPOTPTFGGCTKV 146
Qy 133 EIKRTVAAPSVSQGGSGGGGSGGSGGQVQVLSGGGQVQPGRSRLRS 192
Db 147 EIKS-----SGGSGSGGGSGGGGSEVQLVESGGGVQPGRSRLRSCSSSGFTSDNY 199
Qy 193 MHWYRQALGKLEWVAVISYDGSSTKYAASVKGRFTISRDTSKNTVYKMSLRTEDPAY 252
Db 200 MYWYRQALGKLEWVAVISYDGSSTKYAASVKGRFTISRDTSKNTVYKMSLRTEDPAY 259
Qy 253 YTCARDQSLGDYDHYGLDWKGGTTVYSSG-----SEQKLISEEDLN 297
Db 260 YFCAR-----GYRYREGAMDYWGQGTPTVSSPRLQVDEQKLISEEDLN 303
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RESULT 6

US-10-634-862-11

; Sequence 11, Application US/10634862

; Publication No. US20040048383A1

; GENERAL INFORMATION:

; APPLICANT: RUDERT, FRITZ

; APPLICANT: GE, LIMING

APPLICANT: ILAG, VIC  
TITLE OF INVENTION: NOVEL METHOD AND PHAGE FOR THE IDENTIFICATION OF  
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING MEMBERS OF A MULTIMERIC  
FILE OF INVENTION: (POLY) PEPTIDE COMPLEX  
FILE REFERENCE: MORPHO/9  
CURRENT APPLICATION NUMBER: US/10/634,862  
CURRENT FILING DATE: 2003-08-06  
PRIOR APPLICATION NUMBER: US/09/495,880A  
PRIOR FILING DATE: 2000-02-01  
PRIOR APPLICATION NUMBER: PCT/EP98/04836  
PRIOR FILING DATE: 1998-08-03  
PRIOR APPLICATION NUMBER: EP 97 11 3319.4  
PRIOR FILING DATE: 1997-08-01  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 11  
LENGTH: 456  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: ompA-FLAG-scFv (anti-  
OTHER INFORMATION: HAQ)-gene iliss encoded by phage vector fha91a (circular)  
US-10-634-862-11

Query Match 58.6%; Score 926.5; DB 15; Length 456;  
Best Local Similarity 63.1%; Pred. No. 1.3e-52;  
Matches 190; Conservative 37; Mismatches 49; Indels 25; Gaps 6;

QY 3 MKKTAIAIAVALAGPATAQA---DIVLTQSPGTLISLSPGERATLSCRAQSQSSS--- 55  
DB 1 MKKTAIAIAVALAGPATAQAADYKDIWMTQSPSLVTAGEKVTMSCTSSQSLFNSGKX 60  
QY 56 -YLAAYQQRGAAPRLIYGASTRATGMPDRFSGSSGSDFTLTISRLEPEFAFYCCQ 114  
DB 61 NLTLYQQPQPPKPLIYMASTRGVDREFTGSGSDFTLTISRVAEPLAVYYCON 120  
QY 115 YGSSPQTPQITFGGKTKVEIKRTVAAP-----VSGGSGSGSGSGSGSGSOVLVS 166  
DB 121 DYSNP-----LTRGGGFKLELKRAGGGSGGGSGGGSGGGSGGGSGGGSEVQLVS 176  
QY 167 GGGVQVQGRSLRLSCAAGFPFRSFAHWWROALGKLEWVAIVSYDSTKTYADSVKGR 226  
DB 177 GGDLYVQGGSLKSLSCAAGFSFSYGMWVRQTPDKRELVATISNGGGYTYPPDSVKGR 236  
QY 227 FTISRDTSKNTLYYIKNSLTREDTAVYICARQSLGDVHDHYGDLWQKGTYYVSSGS 286  
DB 237 FTISRDNAKNTLYIQMSSLSKSEDSAMYICARR-----YDE-NGPAYWQGLTVTSASG 291  
QY 287 E 287  
DB 292 E 292

RESULT 7  
US-09-983-580-6  
Sequence 6, Application US/09983580  
Patent No. US20020151061A1  
GENERAL INFORMATION:  
APPLICANT: Filipula, David R.  
APPLICANT: Wang, Maoliang  
APPLICANT: Whitlow, Marc D.  
TITLE OF INVENTION: No. US20020151061A1 Method for Targeted Delivery of Nucleic Acid  
FILE REFERENCE: 0977.2300002  
CURRENT APPLICATION NUMBER: US/09/983,580  
CURRENT FILING DATE: 2001-10-25  
PRIOR APPLICATION NUMBER: 09/420,592  
PRIOR FILING DATE: 1999-10-19  
PRIOR APPLICATION NUMBER: 60/104,949  
PRIOR FILING DATE: 1998-10-20  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 283

TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Kabat  
OTHER INFORMATION: Consensus  
NAME/KEY: UNSURE  
LOCATION: (232)  
OTHER INFORMATION: May be any amino acid.  
NAME/KEY: UNSURE  
LOCATION: (234)  
OTHER INFORMATION: May be any amino acid.  
NAME/KEY: UNSURE  
LOCATION: (239)  
OTHER INFORMATION: May be any amino acid.  
US-09-983-580-6

Query Match 56.4%; Score 892; DB 9; Length 283;  
Best Local Similarity 66.3%; Pred. No. 1.5e-50;  
Matches 181; Conservative 29; Mismatches 47; Indels 16; Gaps 5;

QY 24 DIVLTQSPGTLISLSPGERATLSCRAQSV--SSYLAAYQQRGAAPRLIYGASTRATG 81  
DB 1 DIQWTSQSPSLASVGDVITTCRAQSGLVSIWLAAYQQRGAAPRLIYAASSLRSG 60  
QY 82 MPDRFSGSGSDFTLTISRLEPEFAFYCCOYQSSPQITFGGKTKVEIKRTVAAP 141  
DB 61 VPSRPSGSGSDFTLTISRLEPEFAFYCCQYNS--LPEWTFGQTKVEIKGS--- 113  
QY 142 SVSGGSGSGSDFTLTISRLEPEFAFYCCOYQSSPQITFGGKTKVEIKRTVAAP 201  
DB 114 --TSGSGKRGSGESTKGEVQLVSGGGLVQPGSLRLSCAAGFTFSYAMSWVRQAPG 171  
QY 202 KGLEWVAIVS--YDSTKTYADSVKGRFTISRDTSKNTLYIKNSLTREDTAVYICARDQ 259  
DB 172 KGLEWVAIVSISGKTGGSYTYADSVKGRFTISRDTSKNTLYIKNSLTREDTAVYICARDQ 231  
QY 260 ---SLLEGDHYGDLWQKGTYYVSSGSBOK 289  
DB 232 XGSLISGKYYHYFDYWGGLTVTSKSKKKK 264

RESULT 8  
US-09-985-442-6  
Sequence 6, Application US/09985442  
Patent No. US20020156248A1  
GENERAL INFORMATION:  
APPLICANT: Filipula, David R.  
APPLICANT: Wang, Maoliang  
APPLICANT: Whitlow, Marc D.  
TITLE OF INVENTION: No. US20020156248A1 Method for Targeted Delivery of Nucleic Acid  
FILE REFERENCE: 0977.2300003  
CURRENT APPLICATION NUMBER: US/09/985,442  
CURRENT FILING DATE: 2001-11-02  
PRIOR APPLICATION NUMBER: 09/420,592  
PRIOR FILING DATE: 1999-10-19  
PRIOR APPLICATION NUMBER: 60/104,949  
PRIOR FILING DATE: 1998-10-20  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 283  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Kabat  
OTHER INFORMATION: Consensus  
NAME/KEY: UNSURE  
LOCATION: (232)  
OTHER INFORMATION: May be any amino acid.  
NAME/KEY: UNSURE  
LOCATION: (234)  
OTHER INFORMATION: May be any amino acid.  
NAME/KEY: UNSURE  
LOCATION: (239)  
OTHER INFORMATION: May be any amino acid.





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Sequence 21, Application US/10409938
Publication No. US20030219733A1
GENERAL INFORMATION:
APPLICANT: Clark et al.
TITLE OF INVENTION: ANTI-BODY GENE TRANSFER AND RECOMBINANT AAV THEREFOR
FILE REFERENCE: 28335/39282
CURRENT APPLICATION NUMBER: US/10/409,938
CURRENT FILING DATE: 2003-04-09
PRIORITY APPLICATION NUMBER: US 60/371,501
PRIORITY FILING DATE: 2002-04-09
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
LENGTH: 279
TYPE: PRT
ORGANISM: Homo sapiens
US-10-409-938-21

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84 DFESGSGCTDEFTITSPIEPDEFAYVYCOOYGSBPOTBOITFEGGKTVEIKRTVAAPSV 143

54.28; Score 857.5; DB 15; Length 279;





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OM protein - protein search, using sw model

Run on: February 18, 2005, 08:46:53, Search time 24 Seconds  
(without alignments)  
1218.746 Million cell updates/sec

Title: US-09-194-164-14  
Perfect score: 1582  
Sequence: 1 EFMKKTALVALALGPAIV.....GSEOKLISEEDLNHHHKL 304

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: PIR 79: \*  
1: PIR1: \*  
2: PIR2: \*  
3: PIR3: \*  
4: PIR4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	541.5	34.2	122	2 E36005	Ig heavy chain V r
2	539.5	34.1	128	2 S48797	Ig heavy chain V r
3	537.5	34.0	215	2 A23746	Ig kappa chain V-I
4	534	33.8	109	2 G30607	Ig kappa chain V-I
5	530	33.5	109	2 A30608	Ig kappa chain V-I
6	530	33.5	109	2 B30601	Ig kappa chain V-I
7	529	33.4	109	2 D30601	Ig kappa chain V-I
8	528.5	33.4	108	2 H44151	Ig kappa chain V r
9	527.5	33.3	215	2 JE0242	Ig kappa chain NIG
10	527	33.3	109	2 C30601	Ig kappa chain V-I
11	526	33.2	109	2 F30607	Ig kappa chain V-I
12	526	33.2	129	1 K3H08A	Ig kappa chain pre
13	525	33.2	123	2 S38493	Ig heavy chain - h
14	525	33.2	129	2 S49532	anti-Sm antibody V
15	524	33.1	109	2 H30601	Ig kappa chain V-I
16	523	33.1	109	1 K3H08T	Ig kappa chain V-I
17	522.5	33.0	114	2 S46375	Ig kappa chain V-I
18	522	33.0	109	2 PH0963	Ig kappa chain V r
19	521	32.9	109	2 G30601	Ig kappa chain V-I
20	520	32.9	129	1 K3H08T	Ig kappa chain pre
21	518	32.7	108	2 C30608	Ig kappa chain V r
22	516	32.6	129	2 S46369	Ig light chain var
23	516	32.6	134	2 S38643	Ig kappa chain V r
24	515	32.6	107	2 PH0965	Ig kappa chain V r
25	514	32.5	108	2 B30608	Ig kappa chain V-I
26	514	32.5	145	2 S20631	Ig kappa chain - h
27	513	32.4	119	2 F30605	Ig heavy chain V r
28	512	32.4	109	2 F30601	Ig kappa chain V-I
29	510.5	32.3	104	2 PH0964	Ig kappa chain V r

30	510	32.2	109	1 K3H08T	Ig kappa chain V-I
31	510	32.2	128	2 S20636	Ig kappa chain V r
32	509	32.1	121	2 G36005	Ig heavy chain V r
33	508	32.1	134	2 S31679	Ig heavy chain V r
34	507.5	32.1	110	2 E30607	Ig kappa chain V-I
35	507.5	32.1	114	2 S46390	Ig heavy chain V r
36	507.5	32.1	147	2 I37780	Ig variable region
37	506	32.0	109	1 K3H08T	Ig kappa chain V-I
38	505	31.9	109	2 F44151	Ig kappa chain V r
39	504.5	31.9	122	2 S31117	Ig heavy chain - h
40	504	31.9	132	2 S31603	Ig heavy chain V r
41	503.5	31.8	108	2 E30609	Ig kappa chain V-I
42	503	31.8	130	2 PH0098	Ig heavy chain pre
43	503	31.8	133	2 A49028	Ig heavy chain V-I
44	502.5	31.8	110	2 S44120	Ig kappa chain V-I
45	502	31.7	121	2 S40327	Ig kappa chain - h

ALIGNMENTS

```
RESULT 1
E36005
Ig heavy chain V region (M72) - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
R:Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A:Reference number: A36005, MUID:90349571, PMID:2117273
A:Accession: E36005
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-122 <SCH>
A:Cross-references: GB:M34030
C:Genetics:
A:Gene: GDB:IGH@; IGHDI1
A:Cross-references: GDB:118731, OMIM:146910
A:Map position: 14q32.33-14q32.33
C:Superfamily: Immunoglobulin V region, Immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IM>

Query Match      34.2%; Score 541.5; DB 2; Length 122;
Best Local Similarity 84.0%; Pred. No. 4.4e-30;
Matches 105; Conservative 6; Mismatches 11; Indels 3; Gaps 1;

Cy      160 QVQLVSGGVPQPSRLSCAASGFPFRSPAMHWVRQALGKLEWYAVISYDGTKY 219
      |||||
Db      1 QVQLVSGGVPQPSRLSCAASGFTFSYAMHWVRQAPKGLWYAVISYDGNKTY 60

Cy      220 ADSVYGRFTISRDTSKNTVYLKMSISRTEDTAVVYCARDSILGSDYHYGSDVWGKGT 279
      |||||
Db      61 ADSVYGRFTISRDTSKNTVYLKMSISRTEDTAVVYCARDSILGSDYHYGSDVWGKGT 117

Cy      280 VTVSS 284
      |||||
Db      118 VTVSS 122

RESULT 2
S48797
Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH6) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Sep-1998 #text_change 23-Jul-1999
R:Maimoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
Submitted to the EMBL Data Library, October 1994
A:Description: Molecular characterization of natural human anti-Sm autoantibodies.
A:Reference number: S48797
A:Accession: S48797
A:Molecule type: mRNA
```

A:Residues: 1-128 <MAH>  
 A:Cross-references: EMBL:246379, NID:g587147, PIDN:CAA86512.1, PID:g1340168  
 R.Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.  
 J. Mol. Biol. 227, 776-798, 1992  
 A:Title: The repertoire of human germ-line V(H) sequences reveals about fifty groups of V  
 A:Reference number: S26885, MUID:93021117, PMID:1404388  
 A:Accession: S26893  
 A:Molecule type: DNA  
 A:Residues: 1-98 <TOM>  
 A:Cross-references: EMBL:212350, NID:g32922, PIDN:CAA78220.1, PID:g32923  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 34.1%; Score 539.5; DB 2; Length 128;  
 Best Local Similarity 82.0%; Pred. No. 6.3e-30;  
 Matches 105; Conservative 6; Mismatches 14; Indels 3; Gaps 1;

QY 160 QVQLVSSGGGVQVQPGKSLRLSCAASGFPFRSPAMHWROALKGLEWVAVISYDSTKYY 219  
 DB 1 QVQLVSSGGGVQVQPGKSLRLSCAASGFTSYGMHWROAPGKLEWVAIVYDGSNKYY 60  
 QY 220 ADSVAGRFITSDTSKNLYLKNNSLRTEDTAVYYCARDQ---SLGDDYHYGLDVGK 276  
 DB 61 ADSVAGRFITSDTSKNLYLQMSLRADTAVYYCARDNYVYDSSGYYYHYGMVWGQ 120  
 QY 277 GTTVTVSS 284  
 DB 121 GTTVTVSS 128

## RESULT 3

A23746  
 Ig kappa chain V-III (Kau cold agglutinin) - human  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 21-Jan-2000  
 C:Accession: A23746  
 R:Leon, J.; Ghiso, J.; Goni, F.; Frangione, B.  
 J. Biol. Chem. 266, 2836-2842, 1991  
 A:Title: The primary structure of the Fab fragment of protein Kau, a monoclonal immunogl  
 A:Reference number: A23746; MUID:91131575; PMID:1993660  
 A:Accession: A23746  
 A:Molecule type: protein  
 A:Status: preliminary  
 A:Residues: 1-215 <LBO>  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 34.0%; Score 537.5; DB 2; Length 215;  
 Best Local Similarity 58.7%; Pred. No. 1.5e-29;  
 Matches 128; Conservative 13; Mismatches 50; Indels 27; Gaps 5;

QY 24 DIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQKQPGQAPRLIYGASTRATGMP 83  
 DB 1 EIVLTQSPATLSLSPGERATLSCASQSVSSSYLAWYQKQPGQAPRLIYGASTRATGIP 60  
 QY 84 DRFGSGSGTPTLTLSRLPEDEFAVYYCQOYGSSPQTPQTTFGGGTVEIKR 143  
 DB 61 DRFGSGSGTPTLTLSRLPEDEFAVYYCQOYGSSP---LTFGGGTVEIKR 116  
 QY 144 SGGGSGGGSGGGGGVQVQPGKSLRLSCAASGFPFRSPAMHW-VAQALGK 202  
 DB 117 FIPFSPDQKSGTASVGL-----NNFYREAKVQMKDNLQGS 157  
 QY 203 GLEWVAIVSYDSTKYVAVYKGRFTISR-DTSKNTVY 239  
 DB 158 GNSGESVTEQDSKOSTY--SLSTLTLSKADYEKKHYV 193

## RESULT 4

G30607  
 Ig kappa chain V-III region (Kas) - human (fragment)

C:Species: Homo sapiens (man)  
 C:Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 21-Jan-2000  
 C:Accession: G30607  
 R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solon  
 J. Immunol. 142, 3158-3163, 1989  
 A:Title: Structural and idiotypic characterization of the L chains of human Igm autoantib  
 A:Reference number: A30601; MUID:89215279; PMID:2496160  
 A:Accession: G30607  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-109 <GON>  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 33.8%; Score 534; DB 2; Length 109;  
 Best Local Similarity 92.0%; Pred. No. 1.3e-29;  
 Matches 104; Conservative 4; Mismatches 1; Indels 4; Gaps 1;

QY 24 DIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQKQPGQAPRLIYGASTRATGMP 83  
 DB 1 DIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQKQPGQAPRLIYGASTRATGIP 60  
 QY 84 DRFGSGSGTPTLTLSRLPEDEFAVYYCQOYGSSPQTPQTTFGGGTVEIKR 136  
 DB 61 DRFGSGSGTPTLTLSRLPEDEFAVYYCQOYGSSP---FTFGGTVEIKR 109

## RESULT 5

A30608  
 Ig kappa chain V-III region (Son) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 09-Jul-2004  
 C:Accession: A30608  
 R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solon  
 J. Immunol. 142, 3158-3163, 1989  
 A:Title: Structural and idiotypic characterization of the L chains of human Igm autoantib  
 A:Reference number: A30601; MUID:89215279; PMID:2496160  
 A:Accession: A30608  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-109 <GON>  
 A:Cross-references: UNIPROT:O9UL78  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 33.5%; Score 530; DB 2; Length 109;  
 Best Local Similarity 92.0%; Pred. No. 2.3e-29;  
 Matches 104; Conservative 4; Mismatches 1; Indels 4; Gaps 1;

QY 24 DIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQKQPGQAPRLIYGASTRATGMP 83  
 DB 1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQKQPGQAPRLIYGASTRATGIP 60  
 QY 84 DRFGSGSGTPTLTLSRLPEDEFAVYYCQOYGSSPQTPQTTFGGGTVEIKR 136  
 DB 61 DRFGSGSGTPTLTLSRLPEDEFAVYYCQOYGSSP---YTFGGGTVEIKR 109

## RESULT 6

B30601  
 Ig kappa chain V-III region (Gio) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 09-Jul-2004  
 C:Accession: B30601  
 R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solon  
 J. Immunol. 142, 3158-3163, 1989  
 A:Title: Structural and idiotypic characterization of the L chains of human Igm autoantib  
 A:Reference number: A30601; MUID:89215279; PMID:2496160  
 A:Accession: B30601  
 A:Status: preliminary  
 A:Molecule type: protein







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